

CTGAGCTGACCTGACCCCCAAAGTGAAGGAGAAGCTGCAAGGGAAAAGGGAGGGACAGAT
 1 -----+-----+-----+-----+-----+-----+ 60
 GACTCGACTGGACTGGGGGTTTCACTTCCTCTTCGACGTTCCCTTTTCCCTCCCTGTCTA

 CAGGGAGACCGGGGAAGAAGGAGGAGCAGCCAAGGAGGCTGCTGTCCCCCACAGAGCAG
 61 -----+-----+-----+-----+-----+-----+ 120
 GTCCCTCTGGCCCCCTTCTTCCTCCTCGTCGGTTCCTCCGACGACAGGGGGGTGTCTCGTC

 CTCGGACTCAGCTCCCGGAGCAACCCAGCTGCGGAGGCAACGGCAGTGCTGCTCCTCCAG
 121 -----+-----+-----+-----+-----+-----+ 180
 GAGCCTGAGTCGAGGGCCTCGTTGGGTTCGACGCCTCCGTTGCCGTACGACGAGGAGGTC

 CGAAGGACAGCAGGCAGGCAGACAGACAGAGGTCCTGGGACTGGAAGGCCTCAGCCCCCA
 181 -----+-----+-----+-----+-----+-----+ 240
 GCTTCCTGTCTCGTCCGTCCGTCTGTCTGTCTCCAGGACCCTGACCTTCCGGAGTCGGGGGT

 GCCACTGGGCTGGGCCTGGCCCAATGGCCTTTAATGACCTCCTGCAGCAGGTGGGGGGTG
 241 -----+-----+-----+-----+-----+-----+ 300
 CGGTGACCCGACCCGGACCGGGTTACCGGAAATTACTGGAGGACGTCGTCCACCCCCCAC

 M A F N D L L Q Q V G G V -

 TCGGCCGCTTCCAGCAGATCCAGGTCACCCTGGTGGTCTCCTCCCCCTGCTCCTGATGGCTT
 301 -----+-----+-----+-----+-----+-----+ 360
 AGCCGGCGAAGGTCGTCTAGGTCCAGTGGGACCACCAGGAGGGGGACGAGGACTACCGAA

 G R F Q Q I Q V T L V V L P L L L M A S -

 CTCACAACACCCTGCAGAACTTCACTGCTGCCATCCCTACCCACCACTGCCGCCCGCCTG
 361 -----+-----+-----+-----+-----+-----+ 420
 GAGTGTGTGGGACGTCTTGAAGTGACGACGGTAGGGATGGGTGGTGACGGCGGGCGGAC

 H N T L Q N F T A A I P T H H C R P P A -

 CCGATGCCAACCTCAGCAAGAACGGGGGGCTGGAGGTCTGGCTGCCCCGGGACAGGCAGG
 421 -----+-----+-----+-----+-----+-----+ 480
 GGCTACGGTTGGAGTCGTTCTTGCCCCCGACCTCCAGACCGACGGGGCCCTGTCCGTCC

 D A N L S K N G G L E V W L P R D R Q G -

 GGCAGCCTGAGTCCTGCCTCCGCTTCACCTCCCCGAGTGGGGACTGCCCTTTCTCAATG
 481 -----+-----+-----+-----+-----+-----+ 540
 CCGTCGGACTCAGGACGGAGGCGAAGTGGAGGGGCGTCACCCCTGACGGGAAAGAGTTAC

 Q P E S C L R F T S P Q W G L P F L N G -

 GCACAGAAGCCAATGGCACAGGGGCCACAGAGCCCTGCACCGATGGCTGGATCTATGACA
 541 -----+-----+-----+-----+-----+-----+ 600
 CGTGTCTTCGGTTACCGTGTCCCCGGTGTCTCGGGACGTGGCTACCGACCTAGATACTGT

 T E A N G T G A T E P C T D G W I Y D N -

 ACAGCACCTTCCCATCTACCATCGTGACTGAGTGGGACCTTGTGTGCTCTCACAGGGCCC
 601 -----+-----+-----+-----+-----+-----+ 660

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TGTCGTGGAAGGGTAGATGGTAGCACTGACTCACCTGGAACACACGAGAGTGTCCCGGG
 S T F P S T I V T E W D L V C S H R A L -
 TACGCCAGCTGGCCAGTCCTTGTACATGGTGGGGTGCTGCTCGGAGCCATGGTGTTCG
 661 -----+-----+-----+-----+-----+ 720
 ATGCGGTTCGACCGGGTCAGGAACATGTACCACCCACGACGAGCCTCGGTACCACAAGC
 R Q L A Q S L Y M V G V L L G A M V F G -
 GCTACCTTGCAGACAGGCTAGGCCGCCGAAGGTACTCATCTTGAACCTGCAGACAG
 721 -----+-----+-----+-----+-----+ 780
 CGATGGAACGTCTGTCCGATCCGGCGGCCTTCCATGAGTAGAACTTGATGGACGTCTGTC
 Y L A D R L G R R K V L I L N Y L Q T A -
 CTGTGTCAGGGACCTGCGCAGCCTTCGCACCCAACCTCCCCATCTACTGCGCCTTCCGGC
 781 -----+-----+-----+-----+-----+ 840
 GACACAGTCCCTGGACGCGTCGGAAGCGTGGGTTGAAGGGTAGATGACGCGGAAGGCCG
 V S G T C A A F A P N F P I Y C A F R L -
 TCCTCTCGGGCATGGCTCTGGCTGGCATCTCCCTCAACTGCATGACACTGAATGTGGAGT
 841 -----+-----+-----+-----+-----+ 900
 AGGAGAGCCCGTACCGAGACCGACCGTAGAGGGAGTTGACGTACTGTGACTTACACCTCA
 L S G M A L A G I S L N C M T L N V E W -
 GGATGCCCATTACACACGGGCCTGCGTGGGCACCTTGATTGGCTATGTCTACAGCCTGG
 901 -----+-----+-----+-----+-----+ 960
 CCTACGGGTAAGTGTGTGCCCGACGCACCCGTGGAACCTAACCGATACAGATGTCCGACC
 M P I H T R A C V G T L I G Y V Y S L G -
 GCCAGTTCCTCCTGGCTGGTGTGGCCTACGCTGTGCCCCACTGGCGCCACCTGCAGCTAC
 961 -----+-----+-----+-----+-----+ 1020
 CGGTCAAGGAGGACCGACCACACCGGATGCGACACGGGGTGACCGCGGTGGACGTGATG
 Q F L L A G V A Y A V P H W R H L Q L L -
 TGGTCTCTGCGCCTTTTTTTTGCCTTCTTCATCTACTCCTGGTTCTTCATTGAGTCGGCCC
 1021 -----+-----+-----+-----+-----+ 1080
 ACCAGAGACGCGGAAAAAACGGAAGAAGTAGATGAGGACCAAGAAGTAACCTCAGCCGGG
 V S A P F F A F F I Y S W F F I E S A R -
 GCTGGCACTCCTCCTCCGGGAGGCTGGACCTCACCTGAGGGCCCTGCAGAGAGTCGCCC
 1081 -----+-----+-----+-----+-----+ 1140
 CGACCGTGAGGAGGAGGCCCTCCGACCTGGAGTGGGACTCCCGGGACGTCTCTCAGCGGG
 W H S S S G R L D L T L R A L Q R V A R -
 GGATCAATGGGAAGCGGAAGAAGGAGCCAAATTGAGTATGGAGGTACTCCGGGCCAGTC
 1141 -----+-----+-----+-----+-----+ 1200

FIGURE 1
 Sheet 2 of 4

CCTAGTTACCCCTTCGCCCTTCTTCCTCGGTTTAACTCATACCTCCATGAGGCCCGGTCAG
 I N G K R E E G A K L S M E V L R A S L -
 TGCAGAAGGAGCTGACCATGGGCAAAGGCCAGGCATCGGCCATGGAGCTGCTGCGCTGCC
 1201 -----+-----+-----+-----+-----+ 1260
 ACGTCTTCCTCGACTGGTACCCGTTTCCGGTCCGTAGCCGGTACCTCGACGACGCGACGG
 Q K E L T M G K G Q A S A M E L L R C P -
 CCACCCTCCGCCACCTCTTCCTCTGCCTCTCCATGCTGTGGTTTGCCACTAGCTTTGCAT
 1261 -----+-----+-----+-----+-----+ 1320
 GGTGGGAGGCGGTGGAGAAGGAGACGGAGAGGTACGACACCAAACGGTGATCGAAACGTA
 T L R H L F L C L S M L W F A T S F A Y -
 ACTATGGGCTGGTCATGGACCTGCAGGGCTTTGGAGTCAGCATCTACCTAATCCAGGTGA
 1321 -----+-----+-----+-----+-----+ 1380
 TGATACCCGACCAGTACCTGGACGTCCCGAAACCTCAGTCGTAGATGGATTAGGTCCACT
 Y G L V M D L Q G F G V S I Y L I Q V I -
 TCTTTGGTGCTGTGGACCTGCCTGCCAAGCTTGTGGGCTTCCTTGTCATCAACTCCCTGG
 1381 -----+-----+-----+-----+-----+ 1440
 AGAAACCACGACACCTGGACGGACGGTTCGAACACCCGAAGGAACAGTAGTTGAGGGACC
 F G A V D L P A K L V G F L V I N S L G -
 GTCGCCGGCCTGCCCAGATGGCTGCACTGCTGCTGGCAGGCATCTGCATCCTGCTCAATG
 1441 -----+-----+-----+-----+-----+ 1500
 CAGCGGCCGGACGGGTCTACCGACGTGACGACGACCGTCCGTAGACGTAGGACGAGTTAC
 R R P A Q M A A L L L A G I C I L L N G -
 GGGTGATACCCAGGACCAGTCCATTGTCCGAACCTCTCTTGCTGTGCTGGGGAAGGGTT
 1501 -----+-----+-----+-----+-----+ 1560
 CCCACTATGGGGTCTCTGGTCAGGTAACAGGCTTGGAGAGAACGACACGACCCCTTCCCAA
 V I P Q D Q S I V R T S L A V L G K G C -
 GTCTGGCTGCCTCCTTCAACTGCATCTTCCTGTATACTGGGGAACCTGTATCCCAATGA
 1561 -----+-----+-----+-----+-----+ 1620
 CAGACCGACGAGGAAGTTGACGTAGAAGGACATATGACCCCTTGACATAGGGTGTTACT
 L A A S F N C I F L Y T G E L Y P T M I -
 TCCGGCAGACAGGCATGGGAATGGGCAGCACCATGGCCCCGAGTGGGCAGCATCGTGAGCC
 1621 -----+-----+-----+-----+-----+ 1680
 AGGCCGTCTGTCCGTACCCTTACCCGTCGTGGTACCGGGCTACCCGTCGTAGCACTCGG
 R Q T G M G M G S T M A R V G S I V S P -
 CACTGGTGAGCATGACTGCCGAGCTCTACCCCTCCATGCCTCTCTTCATCTACGGTGCTG
 1681 -----+-----+-----+-----+-----+ 1740

FIGURE 1
 Sheet 3 of 4

GTGACCACTCGTACTGACGGCTCGAGATGGGGAGGTACGGAGAGAAGTAGATGCCACGAC
 L V S M T A E L Y P S M P L F I Y G A V -
 TTCCTGTGGCCGCCAGCGCTGTCACTGTCCTCCTGCCAGAGACCCTGGGCCAGCCACTGC
 1741 -----+-----+-----+-----+-----+ 1800
 AAGGACACCGGCGGTGCGGACAGTGACAGGAGGACGGTCTCTGGGACCCGGTCGGTGACG
 P V A A S A V T V L L P E T L G Q P L P -
 CAGACACGGTGCAGGACCTGGAGAGCAGGAAAGGGAAACAGACGCGACAGCAACAAGAGC
 1801 -----+-----+-----+-----+-----+ 1860
 GTCTGTGCCACGTCTGACCTCTCGTCCTTTCCCTTTGTCTGCGCTGTCGTTGTTCTCG
 D T V Q D L E S R K G K Q T R Q Q Q E H -
 ACCAGAAGTATATGGTCCCCTGACGGCCTCAGCACAAGAGAAGAATGGACTCTGAGGAC
 1861 -----+-----+-----+-----+-----+ 1920
 TGGTCTTCATATAACCAGGGTGACGTCCGGAGTCGTGTTCTCTTCTTACCTGAGACTCCTG
 Q K Y M V P L Q A S A Q E K N G L *
 TGAGAAGGGGCCTTACAGAACCCTAAAGGGAGGGAAGGTCTACAGGTCTCCGGCCACCC
 1921 -----+-----+-----+-----+-----+ 1980
 ACTCTTCCCCGGAATGTCTTGGGATTTCCCTCCCTTCCAGGATGTCCAGAGGCCGGTGGG
 ACACAAGGAGGAGGAAGAGGAAATGGTGACCCAAGTGTGGGGGTGTTGGTTTCAGGAAAGC
 1981 -----+-----+-----+-----+-----+ 2040
 TGTGTTCTCCTCCTTCTCCTTTACCACTGGGTTCACACCCCAACACCAAGTCCTTTTCG
 ATCTTCCCAGGGGTCCACCTCCCTTTATAAACCCCAACAGAACCATCATTAAAAGGTT
 2041 -----+-----+-----+-----+-----+ 2100
 TAGAAGGGTCCCCAGGTGGAGGGAATATTTGGGGTGGTCTTGGTGTAGTAATTTCCAA
 TGACTGCGCACCAAAAAAAAAAAAAA
 2101 -----+-----+-----+-----+ 2127
 ACTGACGCGTGGTTTTTTTTTTTTTTT

CTGCACCTGAAGCATTGTTGGTGGGTGAGCAGCATGGGCTTTGAGGAGCTGCTGGAGCAGGT
 1 -----+-----+-----+-----+-----+ 60
 GACGTGGACTTCGTAAACCACCCACTCGTCGTACCCGAAACTCCTCGACGACCTCGTCCA

 M G F E E L L E Q V -

 GGGCGGCTTTGGGCCCTTCCAAGTGCAGGATGTGGCACTGCTGGCCCTGCCCCGAGTGCT
 61 -----+-----+-----+-----+-----+ 120
 CCGGCCGAAACCCGGGAAGGTGACGCCTTACACCGTGACGACCGGGACGGGGCTCACGA

 G G F G P F Q L R N V A L L A L P R V L -

 GCTACCACTGCACTTCCTCCTGCCCATCTTCCTGGCTGCCGTGCCCTGCCACCGATGTGC
 121 -----+-----+-----+-----+-----+ 180
 CGATGGTGACGTGAAGGAGGACGGGTAGAAGGACCGACGGCACGGGTGGCTACACG

 L P L H F L L P I F L A A V P A H R C A -

 CCTGCCGGGTGCCCTGCCAAGTTCAGCCATCAGGATGTGTGGCTGGAGGCCCATCTTCC
 181 -----+-----+-----+-----+-----+ 240
 GGACGGCCACGGGGACGGTTGAAGTCGGTAGTCCTACACACCGACCTCCGGGTAGAAGG

 L P G A P A N F S H Q D V W L E A H L P -

 CCGGGAGCCTGATGGCACGCTCAGCTCCTGCCTCCGCTTTGCCTATCCCCAGGCTCTCCC
 241 -----+-----+-----+-----+-----+ 300
 GGCCCTCGGACTACCGTGCGAGTCGAGGACGGAGGCGAAACGGATAGGGGTCCGAGAGGG

 R E P D G T L S S C L R F A Y P Q A L P -

 CAACACCACGTTGGGGGAAGAAAGGCAGAGCCGTGGGGAGCTGGAGGATGAACCTGCCAC
 301 -----+-----+-----+-----+-----+ 360
 GTTGTGGTGCAACCCCTTCTTCCGTCTCGGCACCCCTCGACCTCCTACTTGGACGGTG

 N T T L G E E R Q S R G E L E D E P A T -

 AGTGCCTGCTCTCAGGGCTGGGAGTACGACCACTCAGAATTCTCCTCTACCATTGCAAC
 361 -----+-----+-----+-----+-----+ 420
 TCACGGGACGAGAGTCCCGACCCTCATGCTGCTGAGTCTTAAGAGGAGATGGTAACGTTG

 V P C S Q G W E Y D H S E F S S T I A T -

 TGAGTGGGATCTGGTGTGTGAGCAGAAAGGTCTGAACAGAGCTGCGTCCACTTTCTTCTT
 421 -----+-----+-----+-----+-----+ 480
 ACTCACCTAGACCACACACTCGTCTTCCAGACTTGTCTCGACGCAGGTGAAAGAAGAA

 E W D L V C E Q K G L N R A A S T F F F -

 CGCCGGTGTGCTGGTGGGGGCTGTGGCCTTTGGATATCTGTCCGACAGGTTTGGGCGGCG
 481 -----+-----+-----+-----+-----+ 540
 GCGGCCACACGACCAACCCCGACACCGGAAACCTATAGACAGGCTGTCCAAACCCGCCGC

 A G V L V G A V A F G Y L S D R F G R R -

FIGURE 2

541 GCGTCTGCTGCTGCTAGCCTACGTGAGTACCCTGGTGCTGGGCCTGGCATCTGCAGCCTC
 -----+-----+-----+-----+-----+ 600
 CGCAGACGACGACCATCGGATGCACTCATGGGACCACGACCCGGACCGTAGACGTGGAG

 R L L L V A Y V S T L V L G L A S A A S -

 CGTCAGCTATGTAATGTTTGCCATCACCCGCACCCTTACTGGCTCAGCCCTGGCTGGTTT
 601 -----+-----+-----+-----+-----+ 660
 GCAGTCGATACATTACAAACGGTAGTGGGCGTGGAATGACCGAGTCGGGACCGACCAA

 V S Y V M F A I T R T L T G S A L A G F -

 TACCATCATCGTGATGCCACTGGAGCTGGAGTGGCTGGATGTGGAGCACCGCACCGTGGC
 661 -----+-----+-----+-----+-----+ 720
 ATGGTAGTAGCACTACGGTGACCTCGACCTCACCGACCTACACCTCGTGGCGTGGCACCG

 T I I V M P L E L E W L D V E H R T V A -

 TGGAGTCCTGAGCAGCACCTTCTGGACAGGGGGCGTGATGCTGCTGGCACTGGTTGGGTA
 721 -----+-----+-----+-----+-----+ 780
 ACCTCAGGACTCGTCGTGGAAGACCTGTCCCCGCACTACGACGACCGTGACCAACCCAT

 G V L S S T F W T G G V M L L A L V G Y -

 CCTGATACGGGACTGGCGATGGCTTCTGCTAGCTGTCACCCTGCCTTGTGCCCAAGCAT
 781 -----+-----+-----+-----+-----+ 840
 GGACTATGCCCTGACCGCTACCGAAGACGATCGACAGTGGGACGGAACACGGGGTTCGTA

 L I R D W R W L L L A V T L P C A P S I -

 CCTCAGCCTCTGGTGGGTGCCTGAGTCTGCACGCTGGCTTCTGACCCAAGGCCATGTGAA
 841 -----+-----+-----+-----+-----+ 900
 GGAGTCGGAGACCACCCACGGACTCAGACGTGCGACCGAAGACTGGGTTCCGGTACACTT

 L S L W W V P E S A R W L L T Q G H V K -

 AGAGGCCCCACAGGTACTTGCTCCACTGTGCCAGGCTCAATGGGCGGCCAGTGTGTGAGGA
 901 -----+-----+-----+-----+-----+ 960
 TCTCCGGGTGTCCATGAACGAGGTGACACGGTCCGAGTTACCCGCCGGTCACACACTCCT

 E A H R Y L L H C A R L N G R P V C E D -

 CAGCTTCAGCCAGGAGGCTGTGAGCAAAGTGGCCGCCGGGGAACGGGTGGTCCGAAGACC
 961 -----+-----+-----+-----+-----+ 1020
 GTCGAAGTCGGTCCCTCCGACACTCGTTTACCGGCGGCCCTTGCCCACCAGGCTTCTGG

 S F S Q E A V S K V A A G E R V V R R P -

 TTCATACCTAGACCTGTTCCGCACACCACGGCTCCGACACATCTCACTGTGCTGCGTGGT
 1021 -----+-----+-----+-----+-----+ 1080
 AAGTATGGATCTGGACAAGCGTGTGGTGCCGAGGCTGTGTAGAGTGACACGACGCACCA

 S Y L D L F R T P R L R H I S L C C V V -

FIGURE 2

1081 GGTGTGGTTCGGAGTGAAGTCTCTCTATTACGGCCTGAGTCTGGATGTGTCTGGGGCTGGG
 -----+-----+-----+-----+-----+ 1140
 CCACACCAAGCCTCACTTGAAGAGGATAATGCCGGACTCAGACCTACACAGCCCCGACCC

 V W F G V N F S Y Y G L S L D V S G L G -

 1141 GCTGAACGTGTACCAGACACAGCTGTTGTTCTGGGGCTGTGGAAGTGGCCTCCAAGCTGCT
 -----+-----+-----+-----+-----+ 1200
 CGACTTGACATGGTCTGTGTCTGACAACAAGCCCCGACACCTTGACGGGAGGTTTCGACGA

 L N V Y Q T Q L L F G A V E L P S K L L -

 1201 GGTCTACTTGTCTGGTGGCTACGCAGGACGCCGCCCTCACGCAAGCCGGGACACTGCTGGG
 -----+-----+-----+-----+-----+ 1260
 CCAGATGAACAGCCACGCGATGCGTCTGCGGCGGAGTGGCTTCGGCCCTGTGACGACCC

 V Y L S V R Y A G R R L T Q A G T L L G -

 1261 CACGGCCCTGGCGTTCGGCACTAGACTGCTAGTGTCTCCGATATGAAGTCTTGAGCAC
 -----+-----+-----+-----+-----+ 1320
 GTGCCGGGACCGCAAGCCGTGATCTGACGATCACAGGAGGCTATACTTCAGGACCTCGTG

 T A L A F G T R L L V S S D M K S W S T -

 1321 TGTCTTGGCAGTGATGGGGAAAGCTTTTCTGAAGCTGCCTTCACCACTGCCTACCTGTT
 -----+-----+-----+-----+-----+ 1380
 ACAGGACCGTCACTACCCCTTTCGAAAAAGACTTCGACGGAAGTGGTGACGGATGGACAA

 V L A V M G K A F S E A A F T T A Y L F -

 1381 CACTTCAGAGTTGTACCCTACGGTGCTCAGACAGACAGGGATGGGGCTGACTGCACTGGT
 -----+-----+-----+-----+-----+ 1440
 GTGAAGTCTCAACATGGGATGCCACGAGTCTGTCTGTCCCTACCCCGACTGACGTGACCA

 T S E L Y P T V L R Q T G M G L T A L V -

 1441 GGGCCGGCTGGGGGGCTCTTTGGCCCCACTGGCGGCCTTGCTGGATGGAGTGTGGCTGTC
 -----+-----+-----+-----+-----+ 1500
 CCCGGCCGACCCCCCGAGAAACCGGGGTGACCGCCGGAACGACCTACCTCACACCGACAG

 G R L G G S L A P L A A L L D G V W L S -

 1501 ACTGCCCCAAGCTTACTTATGGGGGGATCGCCCTGCTGGCTGCCGGCACCGCCCTCCTGCT
 -----+-----+-----+-----+-----+ 1560
 TGACGGGTTCGAATGAATACCCCCCTAGCGGGACGACCGACGCGCGTGGCGGGAGGACGA

 L P K L T Y G G I A L L A A G T A L L L -

 1561 GCCAGAGACGAGGCAGGCACAGCTGCCAGAGACCATCCAGGACGTGGAGAGAAAGAGTGC
 -----+-----+-----+-----+-----+ 1620
 CGGTCTCTGCTCCGTCCGTGTCGACGGTCTCTGGTAGGTCCTGCACCTCTCTTTCTCACG

 P E T R Q A Q L P E T I Q D V E R K S A -

FIGURE 2

1621 CCCAACCAGTCTTCAGGAGGAAGAGATGCCCATGAAGCAGGTCCAGAACTAAGTGGGAGT 1680
 -----+-----+-----+-----+-----+-----+
 GGGTTGGTCAGAAGTCTCTCTCTACGGGTACTTCGTCCAGGTCTTGATTACCCCTCA

 P T S L Q E E E M P M K Q V Q N *

 1681 GGAGGCAGGCCCTCCACAGAAGCTCTGCAGCAGGGGCTGGGAGAGCAGAAGGGCAGGCC
 -----+-----+-----+-----+-----+-----+ 1740
 CCTCCGTCCGGGAGGTGTCTTCGAGACGTCTGCCCCGACCCCTCTCGTCTTCCCGTCCGGG

 1741 TGCAACTCAGGCTGGGAGTATCGAACCCTCTGCCTAGGGCCGGAGTTGCTGCCAGTACCC
 -----+-----+-----+-----+-----+-----+ 1800
 ACGTTGAGTCCGACCCCTCATAGCTTGGGAGACGGATCCCGGCCCTAACGACGGTCATGGG

 1801 GCTCCCTCTGCTCATCCATCCTTGATTATTTGGCTTCTAGGAACAGTTGACTTCCCAGAA
 -----+-----+-----+-----+-----+-----+ 1860
 CGAGGGAGACGAGTAGGTAGGAACCTAATAAACCGAAGATCCTTGTCAACTGAAGGGTCTT

 1861 TGCAGTGGGCTGCTGGGCACCCCTCTCACGGTTGGGGAGGATTCTGTAAATAAAGGTGCC
 -----+-----+-----+-----+-----+-----+ 1920
 ACGTCACCCGACGACCCGTGGGGAGAGTGCCAACCCCTCCTAAGACATTTATTTCCACGG

 1921 CCTTGGGTTGGGGCAATGGTGACGAGCTGTGGGAAGAGCCCTGGATAGGAAGCCACTGAG
 -----+-----+-----+-----+-----+-----+ 1980
 GGAACCCAACCCCGTTACCACTGCTCGACACCCCTTCTCGGGACCTATCCTTCGGTGACTC

 1981 TCTGCCCTGGGCTCTGATAAACCTTCACCATTAACCTTGCTGTGTGACCTTGGGCATGTG
 -----+-----+-----+-----+-----+-----+ 2040
 AGACGGGACCCGAGACTATTTTGGAGTGGTAATTGAACGACACACTGGAACCCGTACAC

 2041 GCTTTCCCTCTCTGGCCTCAGTCTGTTTCATCTCCCAAATGGATAATGAAGCCTCTTGGGA
 -----+-----+-----+-----+-----+-----+ 2100
 CGAAAGGGAGAGACCGGAGTCAGACAAGTAGAGGGTTACCTATTACTTCGGAGAACCCT

 2101 GGCCCTACCATAGGATCTGTTGCCATGCTCAAATGAGTTACTGAATAAGGTGCTTCTGCT
 -----+-----+-----+-----+-----+-----+ 2160
 CCGGGATGGTATCCTAGACAACGGTACGAGTTTACTCAATGACTTATTCCACGAAGACGA

 2161 TCTTCTAGAGATGGTGCTAAAGAAAGGACTAGCATATGAGACTTCTGGTACCAATGGGGC
 -----+-----+-----+-----+-----+-----+ 2220
 AGAAGATCTCTACCACGATTTCTTTCTGATCGTATACTCTGAAGACCATGGTTACCCCG

 2221 TGGTGGGCATGCTGTCCACTGTGTGGTGCTAGGACTGCCAATGCCAGGCCCAAGGGACAA
 -----+-----+-----+-----+-----+-----+ 2280
 ACCACCCGTACGACAGGTGACACACCACGATCCTGACGGTTACGGTCCGGGTTCCCTGTT

 2281 AAAGAACAGAGCTTTTTGTTCTCATGGCTGGCCCTGCTACCTCCGAGGCACCCTGCAGGG
 -----+-----+-----+-----+-----+-----+ 2340
 TTTCTTGTCTCGAAAAACAAGGTACCGACCGGGACGATGGAGGCTCCGTGGGACGTCCC

 2341 CAATGCATGTCATCCCAACCCCCACACTCCCCATCCTCCAACCCACTGGTCTCATGCCCA
 -----+-----+-----+-----+-----+-----+ 2400
 GTTACGTACAGTAGGGTTGGGGGTGTGAGGGTAGGAGGTTGGGTGACCAGAGTACGGGT

FIGURE 2

2401 AAGAAGAGTTGAAGGCATGGGAGCCAACATTTTATTGAAGAAGCCACAGAGGCTGAAATT
-----+-----+-----+-----+-----+ 2460
TTCTTCTCAACTTCCGTACCCTCGGTTGTAAAATAACTTCTTCGGTGTCTCCGACTTTAA

CAATAAACACAAGTTTATGAGTAAAAAAAAAAAAAAAAAAAA
2461 -----+-----+-----+-----+ 2501
GTTATTTGTGTTCAAATACTCATTTTTTTTTTTTTTTTTT

FIGURE 2

CTGCACCTGAAGCATTGTTGGTGGGTGAGCAGCATGGGCTTTGAGGAGCTGCTGGAGCAGGT
 1 -----+-----+-----+-----+-----+-----+ 60
 GACGTGGACTTCGTAAACCACCCACTCGTCGTACCCGAAACTCCTCGACGACCTCGTCCA

 M G F E E L L E Q V -

 GGGCGGCTTTGGGCCCTTCCAAGTGCAGGAAATGTGGCACTGCTGGCCCTGCCCCGAGTGCT
 61 -----+-----+-----+-----+-----+-----+ 120
 CCGCCGAAACCCGGGAAGGTTGACGCCTTACACCGTGACGACCGGGACGGGGCTCACGA

 G G F G P F Q L R N V A L L A L P R V L -
 GCTACCACTGCACTTCCTCCTGCCCATCTTCTGGCTGCCGTGCCCTGCCACCGATGTGC
 121 -----+-----+-----+-----+-----+-----+ 180
 CGATGGTGACGTGAAGGAGGACGGGTAGAAGGACCGACGGCACGGGTGGCTACACG

 L P L H F L L P I F L A A V P A H R C A -
 CCTGCCGGGTGCCCCTGCCAACTTCAGCCATCAGGATGTGTGGCTGGAGGCCATCTTCC
 181 -----+-----+-----+-----+-----+-----+ 240
 GGACGGCCACGGGGACGGTTGAAGTCGGTAGTCTACACACCGACCTCCGGGTAGAAGG

 L P G A P A N F S H Q D V W L E A H L P -
 CCGGGAGCCTGATGGCACGCTCAGCTCCTGCCTCCGCTTTGCCTATCCCCAGGCTCTCCC
 241 -----+-----+-----+-----+-----+-----+ 300
 GGCCCTCGGACTACCGTGCGAGTCGAGGACGGAGGCGAAACGGATAGGGTCCGAGAGGG

 R E P D G T L S S C L R F A Y P Q A L P -
 CAACACCACGTTGGGGGAAGAAAGGCAGAGCCGTGGGGAGCTGGAGGATGAACCTGCCAC
 301 -----+-----+-----+-----+-----+-----+ 360
 GTTGTGGTGCAACCCCTTCTTCCGTCTCGGCACCCCTCGACCTCCTACTTGGACGGTG

 N T T L G E E R Q S R G E L E D E P A T -
 AGTGCCTGCTCTCAGGGCTGGGAGTACGACCACTCAGAATTCTCTCTACCATTGCAAC
 361 -----+-----+-----+-----+-----+-----+ 420
 TCACGGGACGAGAGTCCCGACCCCTCATGCTGGTGAGTCTTAAGAGGAGATGGTAACGTTG

 V P C S Q G W E Y D H S E F S S T I A T -
 TGAGTGGGATCTGGTGTGTGAGCAGAAAGGTCTGAACAGAGCTGCGTCCACTTTCTTCTT
 421 -----+-----+-----+-----+-----+-----+ 480
 ACTCACCTAGACCACACACTCGTCTTTCCAGACTTGTCTCGACGCAGGTGAAAGAAGAA

 E W D L V C E Q K G L N R A A S T F F F -
 CGCCGGTGTGCTGGTGGGGGCTGTGGCCTTTGGATATCTGTCCGACAGGTTTGGGCGGCG
 481 -----+-----+-----+-----+-----+-----+ 540
 GCGGCCACACGACCACCCCGACACCGGAAACCTATAGACAGGCTGTCCAAACCCGCCGC

 A G V L V G A V A F G Y L S D R F G R R -

FIGURE 3
 Sheet 1 of 4

GCGTCTGCTGCTGGTAGCCTACGTGAGTACCCTGGTGGCTGGGCCTGGCATCTGCAGCCTC
 541 -----+-----+-----+-----+-----+ 600
 CGCAGACGACGACCATCGGATGCACTCATGGGACCACGACCCGGACCGTAGACGTCCGAG
 R L L L V A Y V S T L V L G L A S A A S -
 CGTCAGCTATGTAATGTTTGCCATCACCCGCACCCTTACTGGCTCAGCCCTGGCTGGTTT
 601 -----+-----+-----+-----+-----+ 660
 GCAGTCGATACATTACAAACGGTAGTGGGCGTGGGAATGACCGAGTCGGGACCGACCAA
 V S Y V M F A I T R T L T G S A L A G F -
 TACCATCATCGTGATGCCACTGGAGCTGGAGTGGCTGGATGTGGAGCACCGCACCGTGGC
 661 -----+-----+-----+-----+-----+ 720
 ATGGTAGTAGCACTACGGTGACCTCGACCTCACCGACCTACACCTCGTGGCGTGGCACCG
 T I I V M P L E L E W L D V E H R T V A -
 TGGAGTCCTGAGCAGCACCTTCTGGACAGGGGGCGTGATGCTGCTGGCACTGGTTGGGTA
 721 -----+-----+-----+-----+-----+ 780
 ACCTCAGGACTCGTCGTGGAAGACCTGTCCCCGCACTACGACGACCGTGACCAACCCAT
 G V L S S T F W T G G V M L L A L V G Y -
 CCTGATACGGGACTGGCGATGGCTTCTGCTAGCTGTACCCTGCCTTGTGCCCCAAGCAT
 781 -----+-----+-----+-----+-----+ 840
 GGACTATGCCCCTGACCGCTACCGAAGACGATCGACAGTGGGACGGAACACGGGGTTCGTA
 L I R D W R W L L L A V T L P C A P S I -
 CCTCAGCCTCTGGTGGGTGCCTGAGTCTGCACGCTGGCTTCTGACCCAAGGCCATGTGAA
 841 -----+-----+-----+-----+-----+ 900
 GGAGTCGGAGACCACCCACGGACTCAGACGTGCGACCGAAGACTGGGTTCGGGTACACTT
 L S L W W V P E S A R W L L T Q G H V K -
 AGAGGCCACAGGTACTTGCTCCACTGTGCCAGGCTCAATGGGCGGCCAGTGTGTGAGGA
 901 -----+-----+-----+-----+-----+ 960
 TCTCCGGGTGTCCATGAACGAGGTGACACGGTCCGAGTTACCCGCCGGTACACACTCCT
 E A H R Y L L H C A R L N G R P V C E D -
 CAGCTTCAGCCAGGAGGCTGTGAGCAAAGTGGCCGCCGGGAACGGGTGGTCCGAAGACC
 961 -----+-----+-----+-----+-----+ 1020
 GTCGAAGTCGGTCTCCGACACTCGTTTCACCGCGGCCCTTGCCACAGGCTTCTGG
 S F S Q E A V S K V A A G E R V V R R P -
 TTCATACCTAGACCTGTTCCGCACACCACGGCTCCGACACATCTCACTGTGCTGCGTGGT
 1021 -----+-----+-----+-----+-----+ 1080
 AAGTATGGATCTGGACAAGGCGTGTGGTGGCGAGGCTGTGTAGAGTGACACGACGCACCA
 S Y L D L F R T P R L R H I S L C C V V -

FIGURE 3
 Sheet 2 of 4

1081 GGTGTGGTTCGGAGTGAACCTTCTCCTATTACGGCCTGAGTCTGGATGTGTCTGGGGCTGGG
 -----+-----+-----+-----+-----+ 1140
 CCACACCAAGCCTCACTTGAAGAGGATAATGCCGGACTCAGACCTACACAGCCCCGACCC

 V W F G V N F S Y Y G L S L D V S G L G -

 1141 GCTGAACGTGTACCAGACACAGCTGTTGTTCTGGGGCTGTGGAACCTGCCCTCCAAGCTGCT
 -----+-----+-----+-----+-----+ 1200
 CGACTTGACATGGTCTGTGTCTGACAACAAGCCCCGACACCTTGACGGGAGGTTTCGACGA

 L N V Y Q T Q L L F G A V E L P S K L L -

 1201 GGTCTACTTGTCTGGTGGCTACGCAGGACGCCGCTCACGCAAGCCGGGACACTGCTGGG
 -----+-----+-----+-----+-----+ 1260
 CCAGATGAACAGCCACGCGATGCGTCTGCGGCGGAGTGCCTTCGGCCCTGTGACGACCC

 V Y L S V R Y A G R R L T Q A G T L L G -

 1261 CACGGCCCTGGCGTTCGGCACTAGACTGCTAGTGTCTCCGATATGAAGTCCTGGAGCAC
 -----+-----+-----+-----+-----+ 1320
 GTGCCGGGACCGCAAGCCGTGATCTGACGATCACAGGAGGCTATACTTCAGGACCTCGTG

 T A L A F G T R L L V S S D M K. S W S T -

 1321 TGTCCTGGCAGTGATGGGGAAAGCTTTTTCTGAAGCTGCCTTCACCACTGCCTACCTGTT
 -----+-----+-----+-----+-----+ 1380
 ACAGGACCGTCACTACCCCTTTGAAAAAGACTTCGACGGAAGTGGTGACGGATGGACAA

 V L A V M G K A F S E A A F T T A Y L F -

 1381 CACTTCAGAGTTGTACCCTACGGTGCTCAGACAGACAGGGATGGGGCTGACTGCACTGGT
 -----+-----+-----+-----+-----+ 1440
 GTGAAGTCTCAACATGGGATGCCACGAGTCTGTCTGTCCCTACCCCGACTGACGTGACCA

 T S E L Y P T V L R Q T G M G L. T A L V -

 1441 GGGCCGGCTGGGGGGCTCTTTGGCCCCACTGGCGGCCTTGCTGGATGGAGTGTGGCTGTCT
 -----+-----+-----+-----+-----+ 1500
 CCCGGCCGACCCCCCGAGAAACCGGGGTGACCGCCGGAACGACCTACCTCACACCGACAG

 G R L G G S L A P L A A L L D G V. W L S -

 1501 ACTGCCCAAGCTTACTTATGGGGGATCGCCCTGCTGGCTGCCGGCACCGCCCTCCTGCT
 -----+-----+-----+-----+-----+ 1560
 TGACGGGTTCGAATGAATACCCCCCTAGCGGGACGACCGACGGCCGTGGCGGGAGGACGA

 L P K L T Y G G I A L L A A G T A L L L -

 1561 GCCAGAGACGAGGCAGGCACAGCTGCCAGAGACCATCCAGGACGTGGAGAGAAAGAGAGA
 -----+-----+-----+-----+-----+ 1620
 CGGTCTCTGCTCCGTCCGTGTCTGACGGTCTCTGGTAGGTCTGACCTCTCTTTCTCTCT

 P E T R Q A Q L P E T I Q D V E R K R D -

FIGURE 3
 Sheet 3 of 4

1621 TGGTGCTAAAGAAAGGACTAGCATATGAGACTTCTGGTACCAATGGGGCTGGTGGGCATG
 -----+-----+-----+-----+-----+ 1680
 ACCACGATTTCTTTCCTGATCGTATACTCTGAAGACCATGGTTACCCCGACCACCCGTAC

 G A K E R T S I *

 1681 CTGTCCACTGTGTGGTGCTAGGACTGCCAATGCCAGGCCCAAGGGACAAAAAGAACAGAG
 -----+-----+-----+-----+-----+ 1740
 GACAGGTGACACACCACGATCCTGACGGTTACGGTCCGGGTTCCTGTTTTTCTTGTCTC

 1741 CTTTTTGTTCATGGCTGGCCCTGCTACCTCCGAGGCACCCTGCAGGGCAATGCATGTC
 -----+-----+-----+-----+-----+ 1800
 GAAAAACAAGAGTACCGACCGGGACGATGGAGGCTCCGTGGGACGTCCCGTTACGTACAG

 1801 ATCCCAACCCCCACACTCCCCATCCTCCAACCCACTGGTCTCATGCCCAAAGAAGAGTTG
 -----+-----+-----+-----+-----+ 1860
 TAGGGTTGGGGGTGTGAGGGGTAGGAGGTGGGTGACCAGAGTACGGGTTTCTTCTCAAC

 1861 AAGGCATGGGAGCCAACATTTTATTGAAGAAGCCACAGAGGCTGAAATTCAATAAACACA
 -----+-----+-----+-----+-----+ 1920
 TTCCGTACCCTCGGTTGTAAAATAACTTCTTCGGTGTCTCCGACTTTAAGTTATTTGTGT

 AGTTTTATGAGTAAAAAAAAAAAAAAAAAAAA
 1921 -----+-----+-----+ 1950
 TCAAAATACTCATTTTTTTTTTTTTTTTTT

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GCAGGGACCTCAACTACACTGATCACCAGCCCCATCGGATCCAGACCCGGCCACCAGTGC
1 -----+-----+-----+-----+-----+-----+-----+ 60
CGTCCCTGGAGTTGATGTGACTAGTGGTCGGGGTAGCCTAGGTCTGGGCCGGTGGTCACG

CATGACCTTCTCGGAGATCCTGGACCGTGTGGGAAGCATGGGCCATTTCCAGTTCCTGCA
61 -----+-----+-----+-----+-----+-----+-----+ 120
GTACTGGAAGAGCCTCTAGGACCTGGCACACCCTTCGTACCCGGTAAAGGTCAAGGACGT

M T F S E I L D R V G S M G H F Q F L H -

TGTAGCCATACTGGGCCTCCCGATCCTCAACATGGCCAACCACAACCTGCTGCAGATCTT
121 -----+-----+-----+-----+-----+-----+-----+ 180
ACATCGGTATGACCCGGAGGGCTAGGAGTTGTACCGGTTGGTGTGGACGACGTCTAGAA

V A I L G L P I L N M A N H N L L Q I F -

CACAGCCGCCACCCCTGTCCACCACTGTGCCCCGCCCCACAATGCCTCCACAGGGCCTTG
181 -----+-----+-----+-----+-----+-----+-----+ 240
GTGTCGGCGGTGGGGACAGGTGGTGACAGCGGGCGGGGTGTTACGGAGGTGTCCCGGAAC

T A A T P V H H C R P P H N A S T G P W -

GGTGCTCCCCATGGGCCCAAATGGGAAGCCTGAGAGGTGCCTCCGTTTTGTACATCCGCC
241 -----+-----+-----+-----+-----+-----+-----+ 300
CCACGAGGGGTACCCGGGTTTACCCTTCGGACTCTCCACGGAGGCAAAACATGTAGGCGG

V L P M G P N G K P E R C L R F V H P P -

CAATGCCAGCCTGCCCAATGACACCCAGAGGGCCATGGAGCCATGCCTGGATGGCTGGGT
301 -----+-----+-----+-----+-----+-----+-----+ 360
GTTACGGTCGGACGGGTTACTGTGGGTCTCCCGGTACCTCGGTACGGACCTACCGACCCA

N A S L P N D T Q R A M E P C L D G W V -

CTACAACAGCACCAAGGACTCCATTGTGACAGAGTGGGACTTGGTGTGCAACTCCAACAA
361 -----+-----+-----+-----+-----+-----+-----+ 420
GATGTTGTCTGTTGTTCTGAGGTAACACTGTCTCACCCTGAACCACACGTTGAGGTTGTT,

Y N S T K D S I V T E W D L V C N S N K -

ACTGAAGGAGATGGCCCAGTCTATCTTCATGGCAGGTATACTGATTGGAGGGCTCGTGCT
421 -----+-----+-----+-----+-----+-----+-----+ 480
TGACTTCCTCTACCGGGTCAGATAGAAGTACCGTCCATATGACTAACCTCCCGAGCACGA

L K E M A Q S I F M A G I L I G G L V L -

TGGAGACCTGTCTGACAGGTTTGGCCGCAGGCCCATCCTGACCTGCAGCTACCTGCTGCT
481 -----+-----+-----+-----+-----+-----+-----+ 540
ACCTCTGGACAGACTGTCCAAACCGGCGTCCGGGTAGGACTGGACGTGATGGACGACGA

G D L S D R F G R R P I L T C S Y L L L -

GGCAGCCAGCGGCTCCGGTGCAGCCTTCAGCCCCACCTTCCCCATCTACATGGTCTTCCG
541 -----+-----+-----+-----+-----+-----+-----+ 600

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FIGURE 4
Sheet 1 of 4

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CCGTCGGTCGCCGAGGCCACGTCGGAAGTCGGGGTGAAGGGGTAGATGTACCAGAAGGC
  A A S G S G A A F S P T F P I Y M V F R -
CTTCCTGTGTGGCTTTGGCATCTCAGGCATTACCCTGAGCACCGTCATCTTGAATGTGGA
601 -----+-----+-----+-----+-----+ 660
GAAGGACACACCGAAACCGTAGAGTCCGTAATGGGACTCGTGGCAGTAGAACTTACACCT
  F L C G F G I S G I T L S T V I L N V E -
ATGGGTGCCTACCCGGATGCGGGCCATCATGTGACAGCACTCGGGTACTGCTACACCTT
661 -----+-----+-----+-----+-----+ 720
TACCCACGGATGGGCCTACGCCCGGTAGTACAGCTGTCTGTAGCCCATGACGATGTGGAA
  W V P T R M R A I M S T A L G Y C Y T F -
TGGCCAGTTCATTCTGCCCCGGCTGGCCTACGCCATCCCCCAGTGGCGTTGGCTGCAGTT
721 -----+-----+-----+-----+-----+ 780
ACCGGTCAAGTAAGACGGGCCGACCGGATGCGGTAGGGGGTCACCGCAACCGACGTCAA
  G Q F I L P G L A Y A I P Q W R W L Q L -
AACTGTGTCCATTCCCTTCTTCGTCTTCTTCCTATCATCCTGGTGGACACCAGAGTCCAT
781 -----+-----+-----+-----+-----+ 840
TTGACACAGGTAAGGGAAGAAGCAGAAGAAGGATAGTAGGACCACCTGTGGTCTCAGGTA
  T V S I P F F V F F L S S W W T P E S I -
ACGCTGGTTGGTCTTGTCTGGAAAGTCCTCGAAGGCCCTGAAGATACTCCGGCGGGTGGC
841 -----+-----+-----+-----+-----+ 900
TGCGACCAACCAGAACAGACCTTTCAGGAGCTTCCGGGACTTCTATGAGGCCGCCACCG
  R W L V L S G K S S K A L K I L R R V A -
TGTCTTCAATGGCAAGAAGGAAGAGGGAGAAAGGCTCAGCTTGGAGGAGCTCAAACCTCAA
901 -----+-----+-----+-----+-----+ 960
ACAGAAGTTACCGTTCTTCCTTCTCCCTCTTCCGAGTCGAACCTCCTCGAGTTTGAGTT
  V F N G K K E E G E R L S L E E L K L N -
CCTGCAGAAGGAGATCTCCTTGGCCAAGGCCAAGTACACCGCAAGTGACCTGTTCCGGAT
961 -----+-----+-----+-----+-----+ 1020
GGACGTCTTCTCTAGAGGAACCGGTTCCGGTTCATGTGGCGTTCACTGGACAAGGCCTA
  L Q K E I S L A K A K Y T A S D L F R I -
ACCCATGCTGCGCCGCATGACCTTCTGTCTTTCCTGGCCTGGTTTGCTACCGGTTTTGC
1021 -----+-----+-----+-----+-----+ 1080
TGGGTACGACGCGCGTACTGGAAGACAGAAAGGGACCGGACCAAACGATGGCCAAAACG
  P M L R R M T F C L S L A W F A T G F A -
CTACTATAGTTTGGCTATGGGTGTGGAAGAATTTGGAGTCAACCTCTACATCCTCCAGAT
1081 -----+-----+-----+-----+-----+ 1140

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FIGURE 4
Sheet 2 of 4

GATGATATCAAACCGATACCCACACCTTCTTAAACCTCAGTTGGAGATGTAGGAGGTCTA
 Y Y S L A M G V E E F G V N L Y I L Q I -
 CATCTTTGGTGGGGTCGATGTCCCAGCCAAGTTCATCACCATCCTCTCCTTAAGCTACCT
 1141 -----+-----+-----+-----+-----+-----+ 1200
 GTAGAAACCACCCAGCTACAGGGTCGGTTCAAGTAGTGGTAGGAGAGGAATTCGATGGA
 I F G G V D V P A K F I T I L S L S Y L -
 GGGCCGGCATAACCACTCAGGCCGCTGCCCTGCTCCTGGCAGGAGGGGCCATCTTGGCTCT
 1201 -----+-----+-----+-----+-----+-----+ 1260
 CCCGGCCGTATGGTGAGTCCGGCGACGGGACGAGGACCGTCCTCCCCGGTAGAACCGAGA
 G R H T T Q A A A L L L A G G A I L A L -
 CACCTTTGTGCCCTTGGACTTGCAGACCGTGAGGACAGTATTGGCTGTGTTGGGAAGGG
 1261 -----+-----+-----+-----+-----+-----+ 1320
 GTGGAAACACGGGAACCTGAACGTCTGGCACTCCTGTCATAACCGACACAAACCTTCCC
 T F V P L D L Q T V R T V L A V F G K G -
 ATGCCTATCCAGCTCCTTCAGCTGCCTCTTCTCTACACAAGTGAATTATACCCACAGT
 1321 -----+-----+-----+-----+-----+-----+ 1380
 TACGGATAGGTCGAGGAAGTCGACGGAGAAGGAGATGTGTTCACTTAATATGGGGTGTCA
 C L S S S F S C L F L Y T S E L Y P T V -
 CATCAGGCAAACAGGTATGGGCGTAAGTAACCTGTGGACCCGCGTGGGAAGCATGGTGTG
 1381 -----+-----+-----+-----+-----+-----+ 1440
 GTAGTCCGTTTGTCCATACCCGCATTTCATTGGACACCTGGGCGCACCTTCGTACCACAG
 I R Q T G M G V S N L W T R V G S M V S -
 CCCGCTGGTGAAAAATCACGGGTGAGGTACAGCCCTTCATCCCCAATATCATCTACGGGAT
 1441 -----+-----+-----+-----+-----+-----+ 1500
 GGGCGACCACTTTTAGTGCCTTCCATGTCGGGAAGTAGGGGTTATAGTAGATGCCCTA
 P L V K I T G E V Q P F I P N I I Y G I -
 CACCGCCCTCCTCGGGGGCAGTGCTGCCCTCTTCCTGCCTGAGACCCTGAATCAGCCCTT
 1501 -----+-----+-----+-----+-----+-----+ 1560
 GTGGCGGGAGGAGCCCCGTCACGACGGGAGAAGGACGGACTCTGGGACTTAGTCGGGAA
 T A L L G G S A A L F L P E T L N Q P L -
 GCCAGAGACTATCGAAGACCTGGAAAAGTGGTCCCTGCGGGCAAAGAAGCCAAAGCAGGA
 1561 -----+-----+-----+-----+-----+-----+ 1620
 CGGTCTCTGATAGCTTCTGGACCTTTTGACCAGGGACGCCCGTTTCTTCGGTTTCGTCCT
 P E T I E D L E N W S L R A K K P K Q E -
 GCCAGAGGTGGAAAAGGCCTCCAGAGGATCCCTCTACAGCCTCACGGACCAGGCCTGGG
 1621 -----+-----+-----+-----+-----+-----+ 1680

FIGURE 4
 Sheet 3 of 4

CGGTCTCCACCTTTTCCGGAGGGTCTCCTAGGGAGATGTCGGAGTGCCTGGTCCGGACCC

P E V E K A S Q R I P L Q P H G P G L G -

CTCCAGCTGAGGACAACGGAACCCCTTTCCCTGCCCTCCAGAGACTGATCCTAGCCAGG

1681 -----+-----+-----+-----+-----+-----+ 1740

GAGGTCGACTCCTGTTGCCTTGGGGGAAAGGGACGGGAGGTCTCTGACTAGGATCGGTCC

S S *

CACCTTAGGAGTATAGGGAGGCCCCATATAGGTCCATCCTCCTAGGATGAAGCCTTCTGA

1741 -----+-----+-----+-----+-----+-----+ 1800

GTGGAATCCTCATATCCCTCCGGGGTATATCCAGGTAGGAGGATCCTACTTCGGAAGACT

GAGCTTGGTGAAGGTGTCTCCATCACCACCACCAGAGCCTCCTGCCCAGCCCTGGCCAGT

1801 -----+-----+-----+-----+-----+-----+ 1860

CTCGAACCACCTTCCACAGAGGTAGTGGTGGTGGTCTCGGAGGACGGGTCGGGACCGGTCA

TCAAAGGTTCAAGCCATCCCTGCCCTTGTCTCCCTGCAACCCAAGCCCTGCCATTCTTC

1861 -----+-----+-----+-----+-----+-----+ 1920

AGTTTCCAAGTTCGGTAGGGACGGGAACAAGAGGGACGTTGGGTTCGGGACGGTAAGAAG

TGTCTAGCCCTTCCCCACTGGCCAACTTCCCCACTGTCCCGGTCTCTTCCCCTGAGGT

1921 -----+-----+-----+-----+-----+-----+ 1980

ACAGATCGGGAAGGGGTGACCGGTTGAAGGGGTGACAGGGCCAGGAGAAGGGGACTCCA

CCCCTGATATCCCCTGGCTCAGTCCTAACAAGACTGAGTCTTAACAAGATGAGAAGTCCT

1981 -----+-----+-----+-----+-----+-----+ 2040

GGGGACTATAGGGGACCGAGTCAGGATTGTTCTGACTCAGAATTGTTCTACTCTTCAGGA

CCCCTTCTTGCTCCACACTTTTCTTTGATGGGAGGTTTCAATAAACAGCGATAAGAAC

2041 -----+-----+-----+-----+-----+-----+ 2100

GGGGAAGAACGGAGGGTGTGAAAAGAACTACCCTCCAAAGTTATTTGTCGCTATTCTTG

TCTAAAAAAAAAAAAAAAAAAAA

2101 -----+-----+-----+-----+-----+-----+ 2121

AGATTTTTTTTTTTTTTTTTTT

CAAATTATTTCTTACGTGACTTTAGAGAAAACGGCTACCTATCTGACCCCAAAACGACTT
 1 -----+-----+-----+-----+-----+ 60
 GTTTAATAAAGAATGCACTGAAATCTCTTTTGCCGATGGATAGACTGGGGTTTTGCTGAA

 GAGGAAACTGTTTCCACGGTCCTGCTGCAGGGGGGAAGCACAGTCGTCAAGAAGAGAGTG
 61 -----+-----+-----+-----+-----+ 120
 CTCCTTTGACAAAGGTGCCAGGACGACGTCCCCCTTCGTGTCAGCAGTTCTTCTCTCAC

 GGGTCAGGATCAAAACACATTTAGTGTGACTTAGGGAAAGAAAACATTTTCCCTCTTTGA
 121 -----+-----+-----+-----+-----+ 180
 CCCAGTCCTAGTTTTGTGTAAATCACACTGAATCCCTTTCTTTGTAAAAGGGAGAAACT

 ACCTCTCTGGATACAGTCATTTTGCCTCTACTTGAGGATCAACTGTTCAACCTCAATGGC
 181 -----+-----+-----+-----+-----+ 240
 TGGAGAGACCTATGTCAGTAAAACGGAGATGAACTCCTAGTTGACAAGTTGGAGTTACCG

 M A -

 CTTTCAGGACCTCCTGGGTCACGCTGGTGACCTGTGGAGATTCCAGATCCTTCAGACTGT
 241 -----+-----+-----+-----+-----+ 300
 GAAAGTCCTGGAGGACCCAGTGCGACCACTGGACACCTCTAAGGTCTAGGAAGTCTGACA

 F Q D L L G H A G D L W R F Q I L Q T V -

 TTTTCTCTCAATCTTTGCTGTTGCTACATACCTTCATTTTATGCTGGAGAACTTCACTGC
 301 -----+-----+-----+-----+-----+ 360
 AAAAGAGAGTTAGAAACGACAACGATGTATGGAAGTAAAATACGACCTCTTGAAGTGACC

 F L S I F A V A T Y L H F M L E N F T A -

 ATTCATACCTGGCCATCGCTGCTGGGTCCACATCCTGGACAATGACACTGTCTCTGACAA
 361 -----+-----+-----+-----+-----+ 420
 TAAGTATGGACCGGTAGCGACGACCCAGGTGTAGGACCTGTTACTGTGACAGAGACTGTT

 F I P G H R C W V H I L D N D T V S D N -

 TGACACTGGGGCCCTCAGCCAAGATGCACTCTTGAGAATCTCCATCCCACTGGACTCAA
 421 -----+-----+-----+-----+-----+ 480
 ACTGTGACCCCGGGAGTCGGTTCTACGTGAGAACTCTTAGAGGTAGGGTGACCTGAGTTT

 D T G A L S Q D A L L R I S I P L D S N -

 CATGAGGCCAGAGAAGTGTCGTCGCTTTGTTTCATCCTCAGTGGCAGCTCCTTCACCTGAA
 481 -----+-----+-----+-----+-----+ 540
 GTACTCCGGTCTCTTCACAGCAGCGAAACAAGTAGGAGTCACCGTCGAGGAAGTGGACTT

 M R P E K C R R F V H P Q W Q L L H L N -

 TGGGACCTTCCCCAACACAAGTGACGCAGACATGGAGCCCTGTGTGGATGGCTGGGTGTA
 541 -----+-----+-----+-----+-----+ 600
 ACCCTGGAAGGGGTTGTGTTCACTGCGTCTGTACCTCGGGACACACCTACCGACCCACAT

 G T F P N T S D A D M E P C V D G W V Y -

FIGURE 5
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TGACAGAATCTCCTTCTCATCCACCATCGGTGACCTGAAGTGGGATCTGGTATGTGACTC
 601 -----+-----+-----+-----+-----+ 660
 ACTGTCTTAGAGGAAGAGTAGGTGGTAGCCACTGGACTTCACCCTAGACCATACACTGAG

 D R I S F S S T I G D L K W D L V C D S -
 TCAATCACTGACTTCAGTGGCTAAATTTGTATTTCATGGCTGGAATGATGTTGGGAGGCAT
 661 -----+-----+-----+-----+-----+ 720
 AGTTAGTGACTGAAGTCACCGATTAAACATAAGTACCGACCTTACTACAACCCTCCGTA

 Q S L T S V A K F V F M A G M M L G G I -
 CTTAGGCGTTCATTTATCAGACAGGTTTGGGAGAAGTTTCGTGCTCAGATGGTGTACCT
 721 -----+-----+-----+-----+-----+ 780
 GAATCCGCAAGTAAATAGTCTGTCCAAACCCTCTTCAAAGCACGAGTCTACCACAATGGA

 L G V H L S D R F G R S F V L R W C Y L -
 CCAGGTTGCCATTGTTGGCACTTGTGCAGCGTTGGCTCCCACTTTCTCATTACTGCTC
 781 -----+-----+-----+-----+-----+ 840
 GGTCCAACGGTAACAACCGTGAACACGTCGCAACCGAGGGTGAAAGGAGTAAATGACGAG

 Q V A I V G T C A A L A P T F L I Y C S -
 AGTACGCTTCTTGTCTGGGATTGCTGCAATGAGCTTCATAACAAATACTATTATGTTAAT
 841 -----+-----+-----+-----+-----+ 900
 TCATGCGAAGAACAGACCCTAACGACGTTACTCGAAGTATTGTTTATGATAATACAATTA

 V R F L S G I A A M S F I T N T I M L I -
 AGCCGAGTGGGCAACACACAGATTCCAGGCCATGGGAATTACATTGGGAATGTGCCCTTC
 901 -----+-----+-----+-----+-----+ 960
 TCGGCTCACCCGTTGTGTGTCTAAGGTCCGGTACCCTTAATGTAACCCTTACACGGGAAG

 A E W A T H R F Q A M G I T L G M C P S -
 TGGTATTGCATTTATGACCCTGGCAGGCCTGGCTTTTGCCATTGAGACTGGCATATCCT
 961 -----+-----+-----+-----+-----+ 1020
 ACCATAACGTAAATACTGGGACCGTCCGGACCGAAAACGGTAAGCTCTGACCGTATAGGA

 G I A F M T L A G L A F A I R D W H I L -
 CCAGCTGGTGGTGTCTGTACCATACTTTGTGATCTTTCTGACCTCAAGTTGGCTGCTAGA
 1021 -----+-----+-----+-----+-----+ 1080
 GGTGACCAACACAGACATGGTATGAAACACTAGAAAGACTGGAGTTCAACCGACGATCT

 Q L V V S V P Y F V I F L T S S W L L E -
 GTCTGCTCGGTGGCTCATTATCAACAATAAACCAGAGGAAGGCTTAAAGGAACCTTAGAAA
 1081 -----+-----+-----+-----+-----+ 1140
 CAGACGAGCCACCGAGTAATAGTTGTTATTTGGTCTCCTTCCGAATTCCTTGAATCTTT

 S A R W L I I N N K P E E G L K E L R K -

FIGURE 5
 Sheet 2 of 4

1141 AGCTGCACACAGGAGTGGAATGAAGAATGCCAGAGACACCCTAACCTGGAGATTTTGAA 1200
 -----+-----+-----+-----+-----+-----+-----+
 TCGACGTGTGTCCTCACCTTACTTCTTACGGTCTCTGTGGGATTGGGACCTCTAAACTT
 A A H R S G M K N A R D T L T L E I L K -
 1201 ATCCACCATGAAAAAAGAACTGGAGGCAGCACAAAAAAAACCTTCTCTGTGTGAAAT 1260
 -----+-----+-----+-----+-----+-----+-----+
 TAGGTGGTACTTTTTCTTGACCTCCGTCGTGTTTTTTTTTTTGAAGAGACACACTTTA
 S T M K K E L E A A Q K K K P S L C E M -
 1261 GCTCCACATGCCCAACATATGTAAAAGGATCTCCCTCCTGTCCTTTACGAGATTTGCAAA 1320
 -----+-----+-----+-----+-----+-----+-----+
 CGAGGTGTACGGGTTGTATACATTTTCTAGAGGGAGGACAGGAAATGCTCTAAACGTTT
 L H M P N I C K R I S L L S F T R F A N -
 1321 CTTTATGGCCTATTTTGGCCTTAATCTCCATGTCCAGCATCTGGGGAACAATGTTTTCCT 1380
 -----+-----+-----+-----+-----+-----+-----+
 GAAATACCGGATAAAACCGGAATTAGAGGTACAGGTCTAGACCCCTTGTTACAAAAGGA
 F M A Y F G L N L H V Q H L G N N V F L -
 1381 GTTGCAGACTCTCTTTGGTGCAGTCATCCTCCTGGCCAACCTGTGTTGCACCTTGGGCACT 1440
 -----+-----+-----+-----+-----+-----+-----+
 CAACGTCTGAGAGAAACCACGTACGTAGGAGGACCGGTTGACACAACGTGGAACCCGTGA
 L Q T L F G A V I L L A N C V A P W A L -
 1441 GAAATACATGAACCGTCGAGCAAGCCAGATGCTTCTCATGTTTCTACTGGCAATCTGCCT 1500
 -----+-----+-----+-----+-----+-----+-----+
 CTTTATGTACTTGGCAGCTCGTTCGGTCTACGAAGAGTACAAGGATGACCGTTAGACGGA
 K Y M N R R A S Q M L L M F L L A I C L -
 1501 TCTGGCCATCATATTTGTGCCACAAGAAATGCAGACGCTGCGTGAGGTTTGGCAACACT 1560
 -----+-----+-----+-----+-----+-----+-----+
 AGACCGGTAGTATAAACACGGTGTCTTTACGTCTGCGACGCACTCCAAACCGTTGTGA
 L A I I F V P Q E M Q T L R E V L A T L -
 1561 GGGCTTAGGAGCGTCTGCTCTTGCCAATACCCTTGCTTTTGCCCATGGAAATGAAGTAAT 1620
 -----+-----+-----+-----+-----+-----+-----+
 CCCGAATCCTCGCAGACGAGAACGGTTATGGGAACGAAACGGGTACCTTTACTTCATTA
 G L G A S A L A N T L A F A H G N E V I -
 1621 TCCCACCATAATCAGGGCAAGAGCTATGGGGATCAATGCAACCTTTGCTAATATAGCAGG 1680
 -----+-----+-----+-----+-----+-----+-----+
 AGGGTGGTATTAGTCCCGTTCTCGATACCCCTAGTTACGTTGGAAACGATTATATCGTCC
 P T I I R A R A M G I N A T F A N I A G -

FIGURE 5
Sheet 3 of 4

1681 AGCCCTGGCTCCCTCATGATGATCCTAAGTGTGTATTCTCCACCCCTGCCCTGGATCAT
 -----+-----+-----+-----+-----+-----+ 1740
 TCGGGACCGAGGGGAGTACTACTAGGATTCACACATAAGAGGTGGGGACGGGACCTAGTA

 A L A P L M M I L S V Y S P P L P W I I -
 CTATGGAGTCTTCCCTTCATCTCTGGCTTTGCTTTCCTCCTCCTTCCTGAAACCAGGAA
 1741 -----+-----+-----+-----+-----+-----+ 1800
 GATACCTCAGAAGGGGAAGTAGAGACCGAAACGAAAGGAGGAGGAAGGACTTTGGTCCTT

 Y G V F P F I S G F A F L L L P E T R N -
 CAAGCCTCTGTTTGGACACCATCCAGGATGAGAAAAATGAGAGAAAAGACCCAGAGAACC
 1801 -----+-----+-----+-----+-----+-----+ 1860
 GTTCGGAGACAAACTGTGGTAGGTCCTACTCTTTTTACTCTCTTTTCTGGGGTCTCTTGG

 K P L F D T I Q D E K N E R K D P R E P -
 AAAGCAAGAGGATCCGAGAGTGGAAGTGACGCAGTTTTTAAGGAATTCCAGGAGCTGACTG
 1861 -----+-----+-----+-----+-----+-----+ 1920
 TTTCTGTTCTCCTAGGCTCTCACCTTCACTGCGTCAAAATTTCCTTAAGGTCCTCGACTGAC

 K Q E D P R V E V T Q F *
 CCGATCAATGAGCCAGATGAAGGGAACAATCAGGACTATTCCTAGACACTAGCAAAA
 1921 -----+-----+-----+-----+-----+-----+ 1977
 GGCTAGTTACTCGGTCTACTTCCCTTGTTAGTCCTGATAAGGATCTGTGATCGTTTT

CTCCTGATAGCAAAAGAACTGAGGAAGCTCTTTCCACTACGGCTGTATTGCACTGGTGAG
 1 -----+-----+-----+-----+-----+-----+ 60
 GAGGACTATCGTTTCTTGACTCCTTCGAGAAAGGTGATGCCGACATAACGTGACCACTC

 TCCGGGCCCCATGGATGAGAAATTGATGCGAGGATCAATACAAGCTTAATTTGAATTAATA
 61 -----+-----+-----+-----+-----+-----+ 120
 AGGCCCGGGTACCTACTCTTTAACTACGCTCCTAGTTATGTTTGAATTAATAATTAT

 AAAGGAAATATTTTCTCCCTTTGAACTTATCTCCGTAAAGCCATTGTGCCTCCTCTTGGG
 121 -----+-----+-----+-----+-----+-----+ 180
 TTTCTTTTATAAAAGAGGGAACTTGAATAGAGGCATTTTCGGTAACACGGAGGAGAACCC

 GGTCACGTGTTTACAATCAATGGCCTTTGAGGAGCTCTTGAGTCAAGTTGGAGGCCTTGG
 181 -----+-----+-----+-----+-----+-----+ 240
 CCAGTGCACAAGTGTAGTTACCGGAACTCCTCGAGAACTCAGTTCAACCTCCGGAACC

 M A F E E L L S Q V G G L G -

 GAGATTTTCAGATGCTTCATCTGGTTTTTATTCTTCCCTCTCTCATGTTATTAATCCCTCA
 241 -----+-----+-----+-----+-----+-----+ 300
 CTCTAAAGTCTACGAAGTAGACCAAAAATAAGAAGGGAGAGAGTACAATAATTAGGGAGT

 R F Q M L H L V F I L P S L M L L I P H -

 TATACTGCTAGAGAACTTTGCTGCAGCCATTCTGGTCATCGTTGCTGGGTCCACATGCT
 301 -----+-----+-----+-----+-----+-----+ 360
 ATATGACGATCTCTTGAAACGACGTCGGTAAGGACCAGTAGCAACGACCCAGGTGTACGA

 I L L E N F A A A I P G H R C W V H M L -

 GGACAATAATACTGGATCTGGTAATGAACTGGAATCCTCAGTGAAGATGCCCTCTTGAG
 361 -----+-----+-----+-----+-----+-----+ 420
 CCTGTTATTATGACCTAGACCATTACTTTGACCTTAGGAGTCACTTCTACGGGAGAACTC

 D N N T G S G N E T G I L S E D A L L R -

 AATCTCTATCCACTAGACTCAAATCTGAGGCCAGAGAAGTGTGCTCGCTTTGTCCATC
 421 -----+-----+-----+-----+-----+-----+ 480
 TTAGAGATAGGGTGATCTGAGTTTAGACTCCGGTCTCTTCACAGCAGCGAAACAGGTAGG

 I S I P L D S N L R P E K C R R F V H P -

 CCAGTGGCAGCTTCTTCACCTGAATGGGACTATCCACAGCACAAGTGAGGCAGACACAGA
 481 -----+-----+-----+-----+-----+-----+ 540
 GGTCAACCGTCGAAGAAGTGGACTTACCCTGATAGGTGTCGTGTTCACTCCGTCTGTGTCT

 Q W Q L L H L N G T I H S T S E A D T E -

 ACCCTGTGTGGATGGCTGGGTATATGATCAAAGCTACTTCCCTTCGACCATTTGTGACTAA
 541 -----+-----+-----+-----+-----+-----+ 600
 TGGGACACACCTACCGACCCATATACTAGTTTCGATGAAGGGAAGCTGGTAACACTGATT

 P C V D G W V Y D Q S Y F P S T I V T K -

FIGURE 6
 Sheet 1 of 5

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GTGGGACCTGGTATGTGATTATCAGTCACTGAAATCAGTGGTTCAATTCCTACTTCTGAC
601 -----+-----+-----+-----+-----+ 660
CACCTTGGACCATACTAATAAGTCAGTGACTTTAGTCACCAAGTTAAGGATGAAGACTG

W D L V C D Y Q S L K S V V Q F L L L T -

TGGAATGCTGGTGGGAGGCATCATAGGTGGCCATGTCTCAGACAGGTTTGGGCGAAGATT
661 -----+-----+-----+-----+-----+ 720
ACCTTACGACCACCCTCCGTAGTATCCACCGGTACAGAGTCTGTCCAAACCCGCTTCTAA

G M L V G G I I G G H V S D R F G R R F -

TATTCTCAGATGGTGTGCTCCAGCTTGCCATTACTGACACCTGCGCTGCCTTCGCTCC
721 -----+-----+-----+-----+-----+ 780
ATAAGAGTCTACCACAAACGAGGTCTGAACGGTAATGACTGTGGACGCGACGGAAGCGAGG

I L R W C L L Q L A I T D T C A A F A P -

CACCTTCCCTGTTTACTGTGTACTACGCTTCTTGGCAGGTTTTTCTTCCATGATCATTAT
781 -----+-----+-----+-----+-----+ 840
GTGGAAGGGACAAATGACACATGATGCGAAGAACCGTCCAAAAAGAAGGTACTAGTAATA

T F P V Y C V L R F L A G F S S M I I I -

ATCAAATAATTCTTTGCCCATTACTGAGTGGATAAGGCCCAACTCTAAAGCCCTGGTAGT
841 -----+-----+-----+-----+-----+ 900
TAGTTTATTAAGAAACGGGTAATGACTCACCTATTCCGGGTTGAGATTTCGGGACCATCA

S N N S L P I T E W I R P N S K A L V V -

AATATTGTCATCTGGTGGCCCTTAGTATTGGACAGATAATCCTGGGAGGCTTGGCTTATGT
901 -----+-----+-----+-----+-----+ 960
TTATAACAGTAGACCACGGGAATCATAACCTGTCTATTAGGACCCCTCCGAACCGAATACA

I L S S G A L S I G Q I I L G G L A Y V -

CTTCCGAGACTGGCAAACCCTGCACGTGGTGGCGTCAGTACCTTTCTTGGCCCTCCTTCT
961 -----+-----+-----+-----+-----+ 1020
GAAGGCTCTGACCGTTTGGGACGTGCACCACCGCAGTCATGGAAAGGAACCGGAGGAAGA

F R D W Q T L H V V A S V P F L G L L L -

CCTTCAAAGGTGGCTGGTGGGAATCTGCTCGGTGGTTGATAATCACCAATAAACTAGATGA
1021 -----+-----+-----+-----+-----+ 1080
GGAAGTTTCCACCGACCACCTTAGACGAGCCACCAACTATTAGTGGTTATTTGATCTACT

L Q R W L V E S A R W L I I T N K L D E -

GGGCTTAAAGGCACTTAGAAAAAGTTGCACGCACAAATGGAATAAAGAATGCTGAAGAAAC
1081 -----+-----+-----+-----+-----+ 1140
CCCGAATTTCCGTGAATCTTTTCAACGTGCGTGTTTACCTTATTTCTTACGACTTCTTTG

G L K A L R K V A R T N G I K N A E E T -

```

FIGURE 6
Sheet 2 of 5

```

CCTGAACATAGAGGTTGTAAGATCCACCATGCAGGAGGAGCTGGATGCAGCACAGACCAA
1141 -----+-----+-----+-----+-----+-----+ 1200
GGACTTGTATCTCCAACATTCTAGGTGGTACGTCCTCCTCGACCTACGTCGTGTCTGGTT

  L N I E V V R S T M Q E E L D A A Q T K -

AACTACTGTGTGTGACTTGTTCGCAACCCAGTATGCGTAAAAGGATCTGTATCCTGGT
1201 -----+-----+-----+-----+-----+-----+ 1260
TTGATGACACACACTGAACAAGGCGTTGGGGTCATACGCATTTTCCTAGACATAGGACCA

  T T V C D L F R N P S M R K R I C I L V -

ATTTTGTAGATTGCAACACAATACCTTTTATGGTACCATGGTCAATCTTCAGCATGT
1261 -----+-----+-----+-----+-----+-----+ 1320
TAAAACTCTAAACGTTTGTGTTATGGAAAATACCATGGTACCAGTTAGAAGTCGTACA

  F L R F A N T I P F Y G T M V N L Q H V -

GGGGAGCAACATTTTCCTGTTGCAGGTACTTTATGGAGCTGTCGCTCTCATAGTTCGATG
1321 -----+-----+-----+-----+-----+-----+ 1380
CCCCTCGTTGTAAAAGGACAACGTCCATGAAATACCTCGACAGCGAGAGTATCAAGCTAC

  G S N I F L L Q V L Y G A V A L I V R C -

TCTTGCTCTTTTGACACTAAATCATATGGGCCGTCGAATAAGCCAGATATTGTTTCATGTT
1381 -----+-----+-----+-----+-----+-----+ 1440
AGAACGAGAAAACGTGATTTAGTATACCCGGCAGCTTATTCGGTCTATAACAAGTACAA

  L A L L T L N H M G R R I S Q I L F M F -

CCTGGTGGGCCTTTCCATTTTGGCCAACACGTTTGTGCCCAAAGAAATGCAGACCCTGCG
1441 -----+-----+-----+-----+-----+-----+ 1500
GGACCACCCGAAAGGTAAAACCGTTGTGCAAACACGGGTTTCTTTACGTCTGGGACGC

  L V G L S I L A N T F V P K E M Q T L R -

TGTGGCTTTGGCATGTCTGGGAATCGGCTGTTCTGCTGCTACTTTTTCCAGTGTGCTGT
1501 -----+-----+-----+-----+-----+-----+ 1560
ACACCGAAACCGTACAGACCCTTAGCCGACAAGACGACGATGAAAAAGGTCACAACGACA

  V A L A C L G I G C S A A T F S S V A V -

TCACTTCATTGAACTCATCCCCACTGTTCTCAGGGCAAGAGCTTCAGGAATAGATTTAAC
1561 -----+-----+-----+-----+-----+-----+ 1620
AGTGAAGTAACTTGAGTAGGGGTGACAAGAGTCCCGTTCTCGAAGTCCTTATCTAAATTG

  H F I E L I P T V L R A R A S G I D L T -

GGCTAGTAGGATTGGAGCAGCACTGGCTCCCCCTCTTGATGACCTTAACGGTATTTTTTAC
1621 -----+-----+-----+-----+-----+-----+ 1680
CCGATCATCCTAACCTCGTCGTGACCGAGGGGAGAACTACTGGAATTGCCATAAAAAATG

  A S R I G A A L A P L L M T L T V F F T -

```

FIGURE 6
Sheet 3 of 5

1681 CACTTTGCCATGGATCATTTATGGAATCTTCCCCATCATTGGTGGCCTTATTGTCTTCCT
 -----+-----+-----+-----+-----+ 1740
 GTGAAACGGTACCTAGTAAATACCTTAGAAGGGTAGTAACCACCGGAATAACAGAAGGA

 T L P W I I Y G I F P I I G G L I V F L -

 1741 CCTACCAGAAACCAAGAATCTGCCTTTGCCTGACACCATCAAGGATGTGGAAAATCAAAA
 -----+-----+-----+-----+-----+ 1800
 GGATGGTCTTTGGTTCTTAGACGGAACGGACTGTGGTAGTTCCTACACCTTTTAGTTTT

 L P E T K N L P L P D T I K D V E N Q K -

 1801 AAAAAATCTCAAGGAAAAGGCATAAAAAATGATTGCTACACAAAAGTGACCAAATTTTAAG
 -----+-----+-----+-----+-----+ 1860
 TTTTITAGAGTTCCTTTTCCGTATTTTACTAACGATGTGTTTTCACTGGTTTAAATTC

 K N L K E K A *

 1861 AAGCCTTCATGAGCTGATTGGTGGGGAAATTCAGAAAAAAAAATACAGGAAAAGAACACA
 -----+-----+-----+-----+-----+ 1920
 TTCGGAAGTACTCGACTAACACCCCTTTAAGTCTTTTTTTTTATGTCCTTTTCTTGTGT

 1921 CCAGAAGGGTTTTTTTCCCTACAACAGCAAGAACATATATTAGATACATGAATCTCAAT
 -----+-----+-----+-----+-----+ 1980
 GGTCTTCCCAAAAAAAGGGATGTTGGTCGTTCTTGTATATAATCTATGTACTTAGAGTTA

 1981 TATAATTATGGCATTAAATTTGCATTTTATTTCAAATTAACCTGTGGGGACATGTAATCT
 -----+-----+-----+-----+-----+ 2040
 ATATTAATACCGTAATTAAACGTAAATAAAGTTTTAATTGAACACCCCTGTACATTAGA

 2041 CTTGAGCAATCTGATATTTTTGGGAAGTCCTTTAAAAAGTTACAAATTTATCAATAAATT
 -----+-----+-----+-----+-----+ 2100
 GAACTCGTTAGACTATAAAAACCCTTCAGGAAATTTTCAATGTTTAAATAGTTATTTAA

 2101 ACTAGTAGATAAGATGATTCAGAAACAAAGGAAAATCACAGAATTAGGATGTGGCTGGCT
 -----+-----+-----+-----+-----+ 2160
 TGATCATCTATTCTACTAAGTCTTTGTTTCCTTTTAGTGTCTTAATCCTACACCGACCGA

 2161 TGGTGTATGAAGCACCATGTGATGAATTCATAAAGTTGCAAAAGTCAAAACAATACTGTA
 -----+-----+-----+-----+-----+ 2220
 ACCACATACTTCGTGGTACACTACTTAAGTATTTCAACGTTTTCAGTTTTGTTATGACAT

 2221 CATGCAACCAGAAATCAAATTAAATCCAGAAATAGAGACCTATATAAATGCATTTAATAC
 -----+-----+-----+-----+-----+ 2280
 GTACGTTGGTCTTTAGTTTAATTTAGGTCTTTATCTCTGGATATATTTACGTAAATTATG

 2281 ATGATACTTTTGACATATTAAGCCATTGGAAAACGGAAGGATTAGATACTTAAATAACAT
 -----+-----+-----+-----+-----+ 2340
 TACTATGAAAACGTATAATTGCGTAACCTTTTGCCTTCCTAATCTATGAATTTATTGTA

 2341 TGCTATCTCTTTGTAAATACAGTCACTAAATGATGTTAGTTACTTTTCCATGGTGGAATT
 -----+-----+-----+-----+-----+ 2400
 ACGATAGAGAAACATTTATGTCAAGTATTTACTACAATCAATGAAAAGGTACCACCTTAA

FIGURE 6
 Sheet 4 of 5

2401 TTAATTACTTTTTCTTTGTAATTTTCTCTCTGTATATTTTAAACAAATAGCTGGTATAG
 -----+-----+-----+-----+ 2460
 AATTAATGAAAAAGAAACATTAAAAAGAGAGACATATAAAATTTGTTTATCGACCATATC

 2461 TTTACAATATTATAAAGATATTGTTCAAATTGAAGGGCAAAGGCCAGGTTTCAGCAATTTT
 -----+-----+-----+-----+ 2520
 AAATGTTATAATATTTCTATAACAAGTTTAACTTCCCGTTTCCGGTCCAAGTCGTTAAAA

 2521 CAAACTGTATGTACATTTAATAAAAATAACTATAAAATTAAAAAATTATATTTCAAATGATG
 -----+-----+-----+-----+ 2580
 GTTTGACATACATGTAAATTATTTATTGATATTTAATTTTTTAATATAAAGTTTACTAC

 2581 TGACTAATAAATGAAAGTACATATAGTAGTAAAGTAATTTTCAGGCAAACCTATATAACCA
 -----+-----+-----+-----+ 2640
 ACTGATTATTTACTTTCATGTATATCATCATTTCAATTAAAGTCCGTTTGGATATATTGGT

 2641 AAATATAAACTTTCATTTTAAACAGCAAAAAAAAAAAAAAAAAAAAAA
 -----+-----+-----+-----+ 2684
 TTTATATTTGAAAGTAAATTTGTCGTTTTTTTTTTTTTTTTTTT

Transport of *p*AH by OAT 1 in HeLa

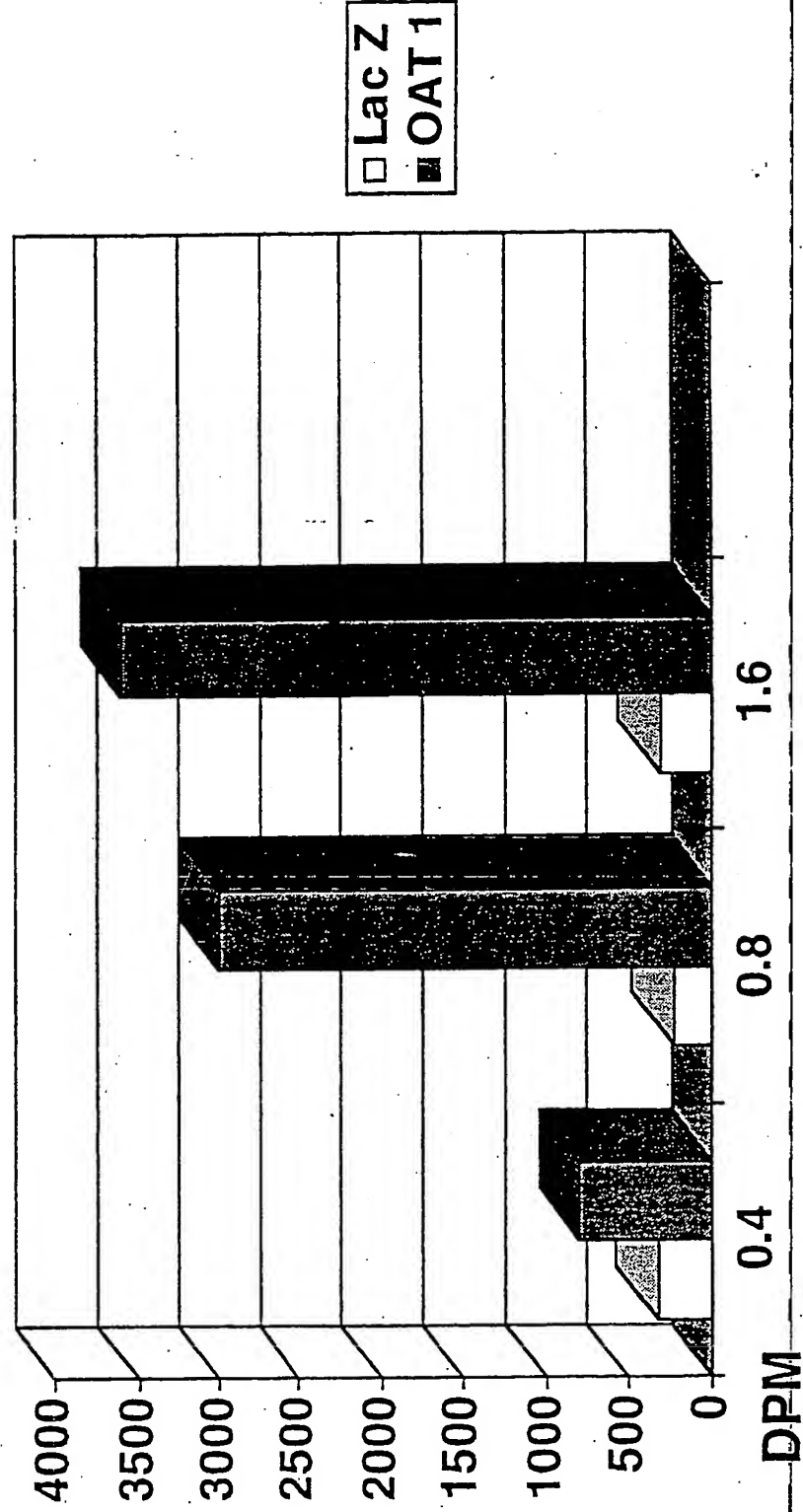


FIGURE 7

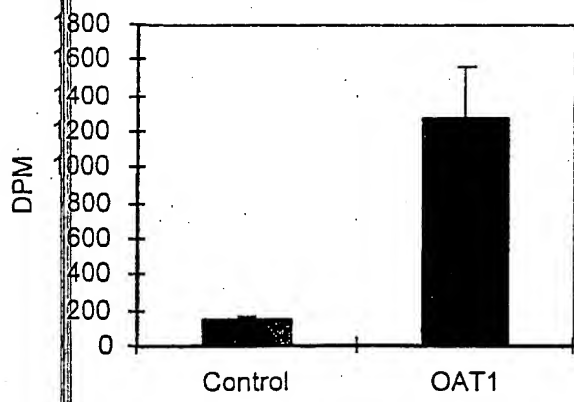


FIGURE 8

PAH Uptake by OAT1 EcR Cell Line

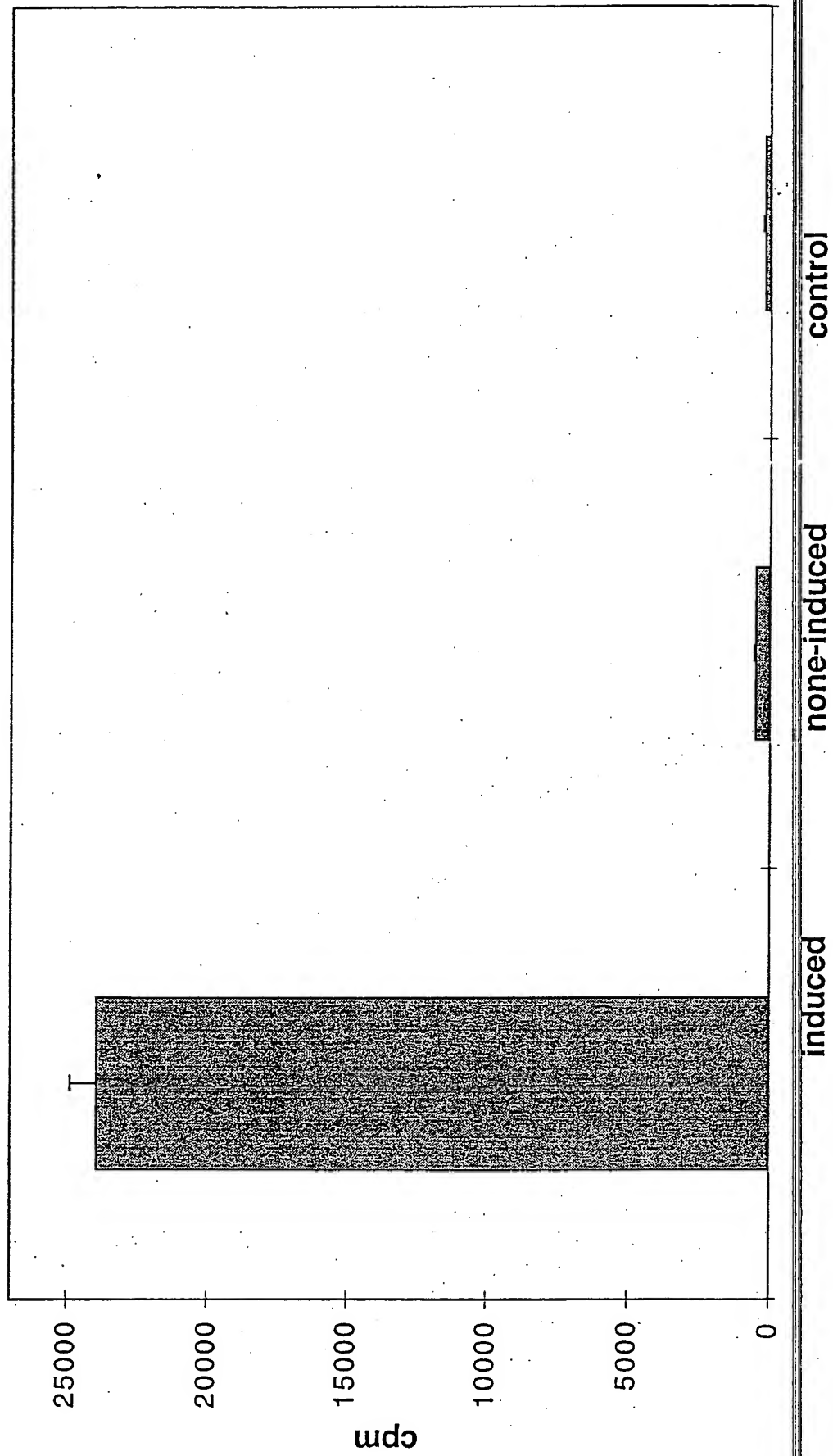


FIGURE 9

PAH Uptake by OAT2 EcR Cell Line

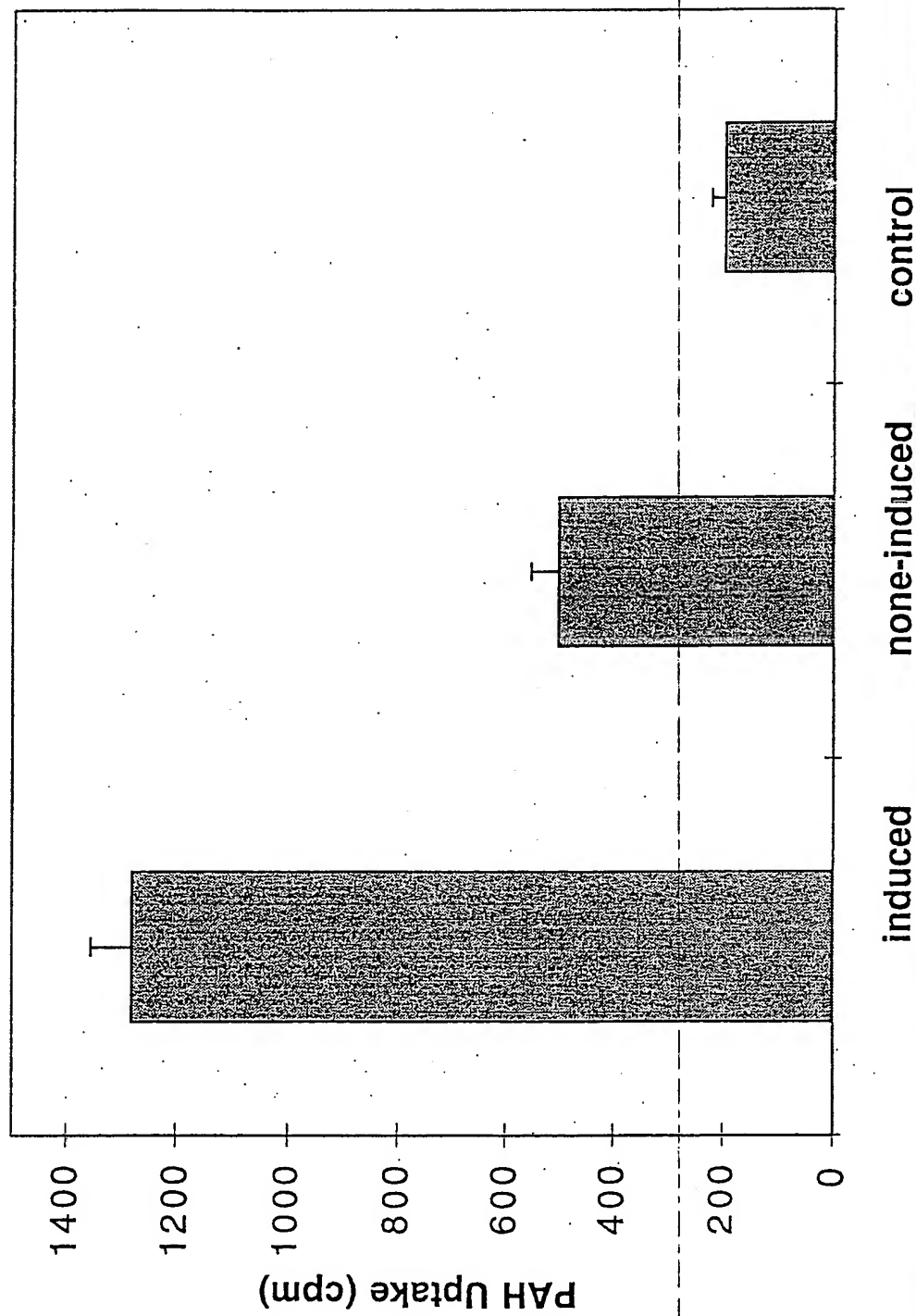


FIGURE 10

PAH Transport by EcR293-OAT2A

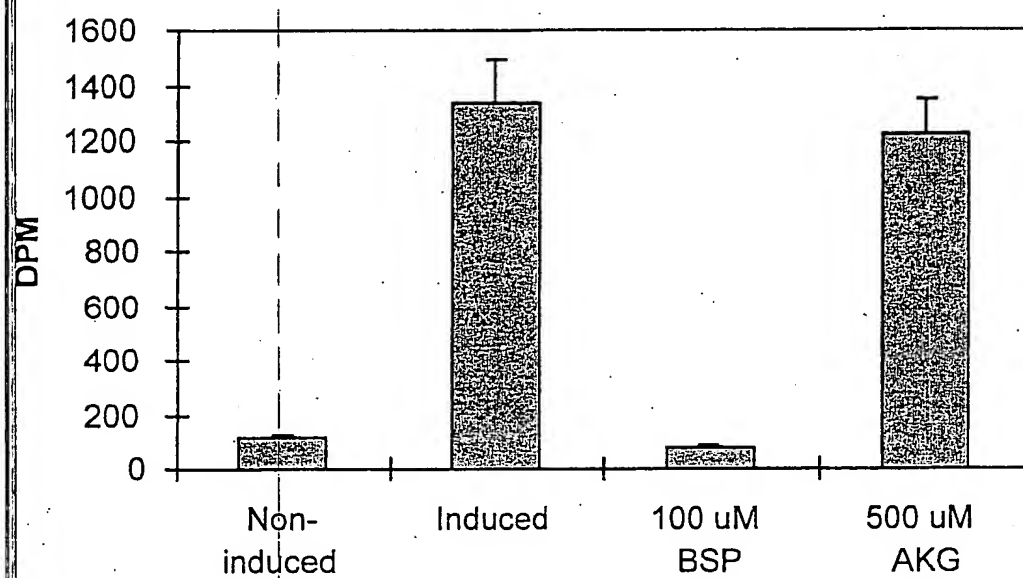


FIGURE 11

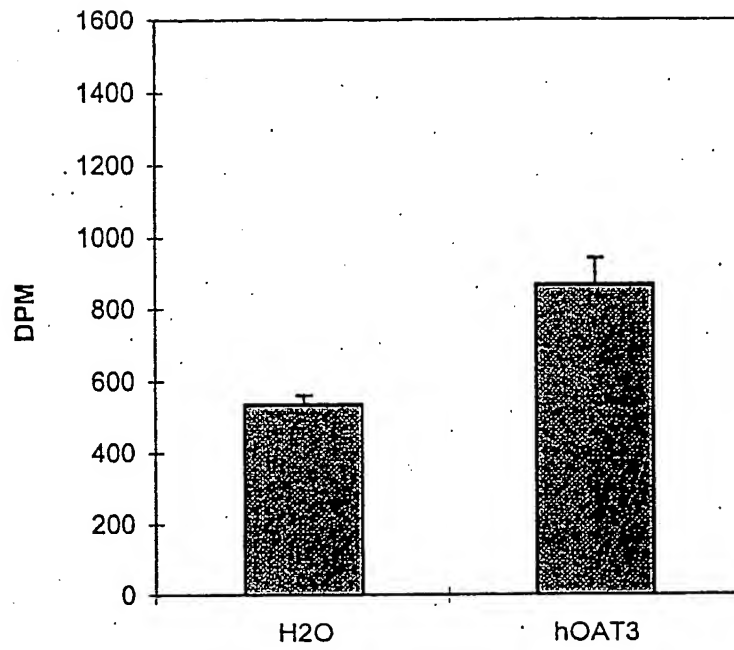


Figure 12: Expression of hOAT3 in *Xenopus* oocytes. Oocytes were injected with either water or hOAT3 complementary RNA and then assayed for uptake of labeled PAH.

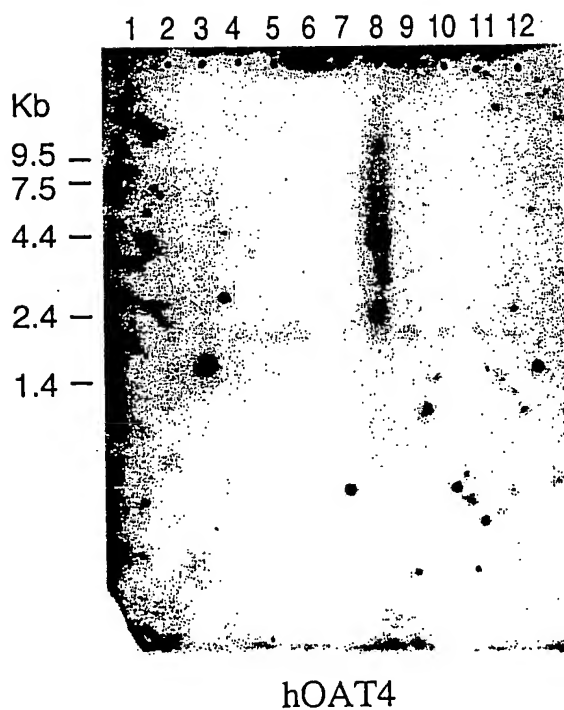
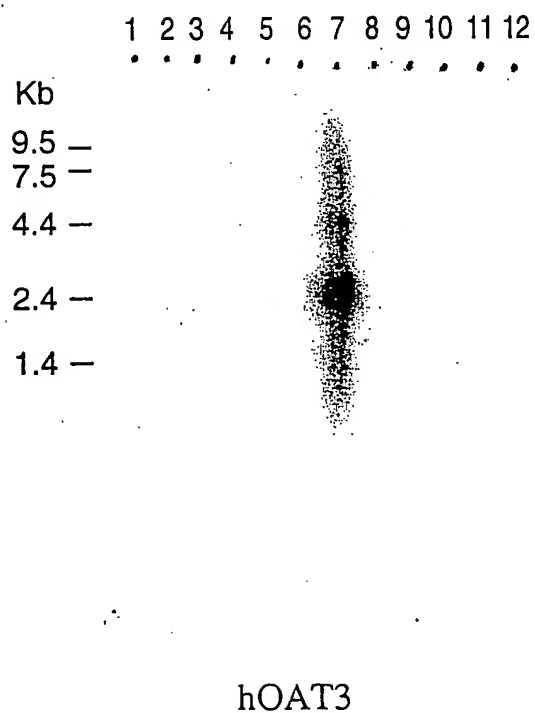
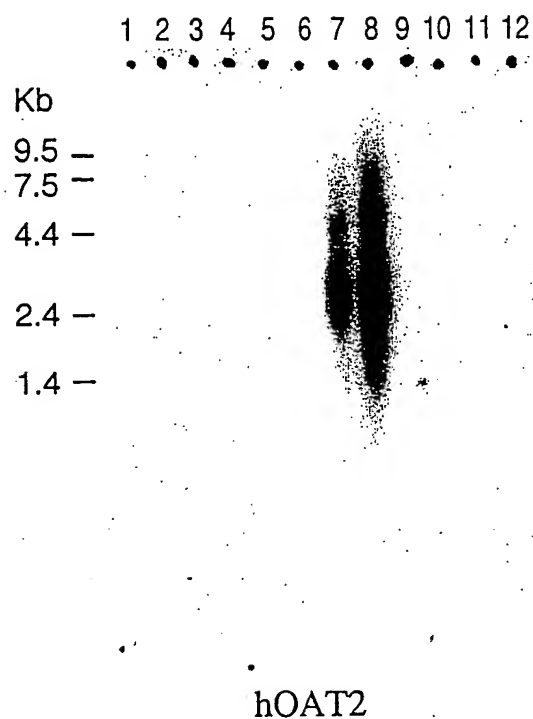
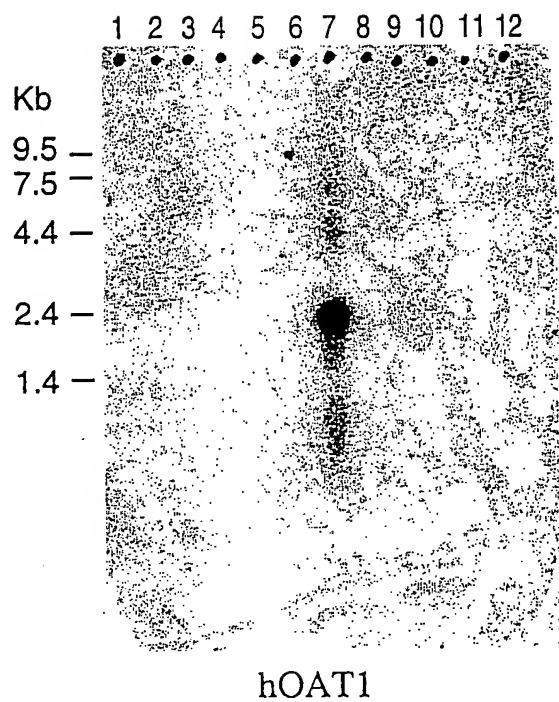


FIGURE 13
Sheet 1 of 2

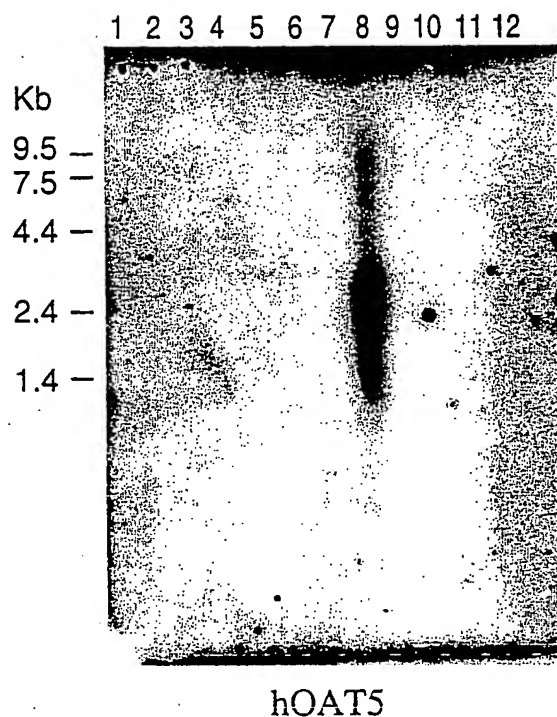


Figure 13: Human Multiple-tissue Northern Blots (Clontech) were hybridized with indicated hOAT cDNAs. Lane numbers corresponds to RNAs extracted from following human tissues:

- | | |
|--------------------|----------------------------------|
| 1. brain | 7. kidney |
| 2. heart | 8. liver |
| 3. skeletal muscle | 9. small intestine |
| 4. colon | 10. placenta |
| 5. thymus | 11. lung |
| 6. spleen | 12. peripheral blood leukocytes. |

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